```
> O <
O|  |O  IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

                -- Outline of search "claim36_pir" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "zara371.key":
  claim36 (AA) ID   claim36 AA preliminary pattern
1       followed by
2         r or n or a or t or v
2         f
2         m or i or t or r or a or s
2         r or h or e or c or s or d
2         h or f or y
2         w
2         e or t or a or f or s
2         g or q or t or a or d
2         f or q or l

Selected files:

       File : claim36pir.pep

                -- Output Parameters --

Format Options:                          File Options:
  Nucleic acid code matching   Exact       Indirect file              No
  Find non-matching hits only  No          Sequence or key file       No
  Report key used              Yes         List of hits               Yes
  Note position of hit         Yes         Hit display                Yes
  Display full annotations     Yes         Name and annotations       Yes
  Sequence context             50

                -- Run Parameters --

  Run mode                     Batch
    Time to start comparison   now
    Notify at end of run       No

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1 match found in sequence:
 s31612 ; TOIG of: s31612  check: 219  from: 1  to: 139
  (from "claim36pir.pep")
  TOIG of: s31612  check: 219  from: 1  to: 139

 P1;S31612 - beta-1,3-glucanase homolog (clone A20) - rape (fragment)
 C;Species: Brassica napus (rape)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Nov-2000
 C;Accession: S31612
 R;Hird, D.; Worrall, D.; Hodge, R.; Paul, W.; Smartt, S.; Draper, J.; Scott, R.
 submitted to the EMBL Data Library, December 1992
 A;Description: The anther-specific protein encoded by the Brassica napus and
  Arabidopsis thaliana A6 gene exhibits homology to beta-1,3-glucanases.
 A;Reference number: S31612
 A;Accession: S31612
 A;Molecule type: mRNA
 A;Residues: 1-139 <HIR>
 A;Cross-references: EMBL:X69889; NID:g17733; PID:g17734
 A;Experimental source: clone A20
 C;Superfamily: beta-1,3-glucanase

   S31612  Length: 139  October 13, 2004 13:40  Type: P  Check: 219  ..
 Found using 'claim36' (zara371.key)

...

                                                              |-------|
49      VWCVAVEGANETELGQALDFACGRSNATCAALAPGRECYAPVSVTWHASYAFSSYWAQFR
                                                             99      107

109     NQSSQCYFNGLARETTTNPGNEQCKFPSVTL

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1 match found in sequence:
 s74688 ; TOIG of: s74688  check: 9387  from: 1  to: 391
  (from "claim36pir.pep")
  TOIG of: s74688  check: 9387  from: 1  to: 391

 P1;S74688 - hypothetical protein sll1200 - Synechocystis sp. (strain PCC 6803)
 C;Species: Synechocystis sp.
 A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C;Accession: S74688
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.;
  Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi,
  T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.;
  Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium
  Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and
  assignment of potential protein-coding regions.
 A;Reference number: S74322; MUID:97061201; PMID:8905231
 A;Accession: S74688
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-391 <KAN>
 A;Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA16839.1;
  PID:d1017572; PID:g1651913
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June
  1996

  S74688  Length: 391  October 13, 2004 13:40  Type: P  Check: 9387  ..
 Found using 'claim36' (zara371.key)

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                                                              |-------|
296     FWLPAIAFSWLLGSSILNNGLIPLLLEILQGNQTGVGIGLYFGCVGLAGDVFTRYWSTQS
                                                             346     354

356     SQMHGGLGLAMLVMSTLLCARYWQGFRVPNKKGAGD

                -- Search Statistics --

Times:                    CPU                  Total Elapsed
                      00:00:00.00              00:00:00.00

Number of sequences searched:                      2
Number of sequence hits:                           2
Number of separate matches:                        2
Number of sequence hits saved:                     0
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> O <
O|  |O  IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

              -- Outline of search "claim36_uni" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "zara371.key":
  claim36 (AA) ID   claim36 AA preliminary pattern
1       followed by
2         r or n or a or t or v
2         f
2         m or i or t or r or a or s
2         r or h or e or c or s or d
2         h or f or y
2         w
2         e or t or a or f or s
2         g or q or t or a or d
2         f or q or l

Selected files:

        File : claim36uni.pep

                    -- Output Parameters --

Format Options:                     File Options:
  Nucleic acid code matching   Exact    Indirect file              No
  Find non-matching hits only  No       Sequence or key file       No
  Report key used              Yes      List of hits               Yes
  Note position of hit         Yes      Hit display                Yes
  Display full annotations     Yes      Name and annotations       Yes
  Sequence context             50


                        -- Run Parameters --

  Run mode                        Batch
    Time to start comparison      now
    Notify at end of run          No

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1 match found in sequence:
 aaq23617 ; LD10322p.
  (from "claim36uni.pep")
  TOIG of: aaq23617  check: 1097  from: 1  to: 1075

 ID   AAQ23617    PRELIMINARY;      PRT;  1075 AA.
 AC   AAQ23617;
 DT   02-MAR-2004 (TrEMBLrel. 27, Created)
 DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE   LD10322p.
 GN   CG16718.
 OS   Drosophila melanogaster (Fruit fly).
 OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC   Ephydroidea; Drosophilidae; Drosophila.
 OX   NCBI_TaxID=7227;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=Berkley;
 RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA   Celniker S.;
 RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
 DR   EMBL; BT010299; AAQ23617.1; -.
 SQ   SEQUENCE   1075 AA;  123934 MW;  729765FBD8339C70 CRC64;

 AAQ23617  Length: 1075  October 13, 2004 13:25  Type: P  Check: 1097  ..
 Found using 'claim36' (zara371.key)

...

                                                                |-------|
451     VPVKDICQSGNTNITMCPLCDWCNFWDLKETCNYAKVTYLIDNPSTVFFAVFMSFWATLF
                                                               501     509

511     LELWKRYSAEITHRWDLTGFDVHEEHPRPQYLARLEHIPPTRVDYVTNI

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1 match found in sequence:
 aaq72537 ; SCL-PHA synthase.
  (from "claim36uni.pep")
  TOIG of: aaq72537  check: 4418  from: 1  to: 566

 ID   AAQ72537    PRELIMINARY;      PRT;   566 AA.
 AC   AAQ72537;
 DT   02-MAR-2004 (TrEMBLrel. 27, Created)
 DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE   SCL-PHA synthase.
 GN   PHAC.
 OS   Pseudomonas sp. HJ-2.
 OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC   Pseudomonadaceae; Pseudomonas.
 OX   NCBI_TaxID=244327;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=HJ-2;
 RA   Seo S.H., Choi G.G., Rhee Y.H.;
 RT   "Cloning of scl-PHA synthase locus and mcl-PHA synthase locus in
 RT   Pseudomonas sp. HJ-2.";
 RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
 DR   EMBL; AY370931; AAQ72537.1; -.
 SQ   SEQUENCE   566 AA;  63672 MW;  F4CBA7A4CE5943F0 CRC64;

 AAQ72537  Length: 566  October 13, 2004 13:25  Type: P  Check: 4418  ..
 Found using 'claim36' (zara371.key)

            |-------|
1       MDNGHTFAHYWSGQAPFIASFVLQQLRLYVAQNTWFSGHDQSQWFDVPVEALEQLQADYQ
              6       14

61      QQWA

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1 match found in sequence:
 cae45695 ; Hypothetical protein.
  (from "claim36uni.pep")
  TOIG of: cae45695  check: 6871  from: 1  to: 180

 ID   CAE45695    PRELIMINARY;      PRT;   180 AA.
 AC   CAE45695;
 DT   02-MAR-2004 (TrEMBLrel. 27, Created)
 DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE   Hypothetical protein.
 OS   Streptomyces parvulus.
 OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC   Streptomycineae; Streptomycetaceae; Streptomyces.
 OX   NCBI_TaxID=146923;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=Tu4055;
```

```
RA   Olano C., Wilkinson B., Sanchez C., Moss S., Sheridan R., Math V.,
RA   Weston A.J., Brana A.F., Martin C. .J., Oliynyk M., Mendez C.,
RA   Leadlay P.F., Salas J.A.;
RT   "Biosynthesis of the angiogenesis inhibitor borrelidin by Streptomyces
RT   parvulu s Tu4055: cluster analysis and assigment of functions.";
RL   Chem. Biol. 11:87-97(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Tu4055;
RA   Olano C., Wilkinson B., Moss S., Brana A.F., Mendez C., Leadlay P.F.,
RA   Salas J.A.;
RT   "Evidence from engineered gene fusions for the repeated use of a
RT   module in a modular polyketide synthase";.";
RL   Chem. Commun. 22:2780-2782(2003).
DR   EMBL; AJ580915; CAE45695.1; -.
KW   Aminotransferase; Hypothetical protein; Oxidoreductase.
SQ   SEQUENCE   180 AA;  19338 MW;  6CCE28A1E48436DB CRC64;

CAE45695  Length: 180  October 13, 2004 13:25  Type: P  Check: 6871  ..
Found using 'claim36' (zara371.key)

...

                                                          |-------|
7       EAAKRVELVFSLFDANGNGVIDSDDFDLMTDRVVAAAAGSDDSAKAAVRAAFRRYWTTLA
                                                        57      65

67      TELDADGDGVITVEEFRPFVLDPERFGPTIAEFARALSALGDPDGDGLI

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1 match found in sequence:
 p72824 ; Sll1200 protein.
  (from "claim36uni.pep")
  TOIG of: p72824  check: 9387  from: 1  to: 391

ID   P72824      PRELIMINARY;      PRT;   391 AA.
AC   P72824;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sll1200 protein.
GN   OrderedLocusNames=sll1200;
OS   Synechocystis sp. (strain PCC 6803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX   NCBI_TaxID=1148;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96127529; PubMed=8590279;
RA   Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA   Sugiura M., Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT   region from map positions 64% to 92% of the genome.";
RL   DNA Res. 2:153-166(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PCC6803;
RX   MEDLINE=97061201; PubMed=8905231;
RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA   Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA   Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT   entire genome and assignment of potential protein-coding regions.";
RL   DNA Res. 3:109-136(1996).
DR   EMBL; D90901; BAA16839.1; -.
DR   PIR; S74688; S74688.
KW   Complete proteome.
SQ   SEQUENCE   391 AA;  42240 MW;  1AFDB350FDED2A45 CRC64;

  P72824  Length: 391  October 13, 2004 13:25  Type: P  Check: 9387  ..
 Found using 'claim36' (zara371.key)

...

                                                                |-------|
296     FWLPAIAFSWLLGSSILNNGLIPLLLEILQGNQTGVGIGLYFGCVGLAGDVFTRYWSTQS
                                                              346     354

356     SQMHGGLGLAMLVMSTLLCARYWQGFRVPNKKGAGD

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1 match found in sequence:
 q06913 ; Beta-1,3-glucanase homologue (Fragment).
  (from "claim36uni.pep")
  TOIG of: q06913  check: 219  from: 1  to: 139

ID   Q06913      PRELIMINARY;      PRT;   139 AA.
AC   Q06913;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-1,3-glucanase homologue (Fragment).
OS   Brassica napus (Rape).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Brassica.
OX   NCBI_TaxID=3708;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94108487; PubMed=8281185;
RA   Hird D.L., Worrall D., Hodge R., Smartt S., Paul W., Scott R.;
RT   "The anther-specific protein encoded by the Brassica napus and
RT   Arabidopsis thaliana A6 gene displays similarity to beta-1,3-
RT   glucanases.";
RL   Plant J. 4:1023-1033(1993).
DR   EMBL; X69889; CAA49515.1; -.
DR   PIR; S31612; S31612.
DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   InterPro; IPR000490; Glyco_hydro_17.
DR   Pfam; PF00332; Glyco_hydro_17; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   139 AA;  14995 MW;  ECBBD63335C551F7 CRC64;

  Q06913  Length: 139  October 13, 2004 13:25  Type: P  Check: 219  ..
 Found using 'claim36' (zara371.key)

...

                                                              |-------|
49      VWCVAVEGANETELGQALDFACGRSNATCAALAPGRECYAPVSVTWHASYAFSSYWAQFR
                                                            99      107

109     NQSSQCYFNGLARETTTNPGNEQCKFPSVTL

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1 match found in sequence:
 q6ufw5 ; SCL-PHA synthase.
  (from "claim36uni.pep")
  TOIG of: q6ufw5  check: 4418  from: 1  to: 566

ID   Q6UFW5      PRELIMINARY;      PRT;   566 AA.
AC   Q6UFW5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   SCL-PHA synthase.
GN   Name=phaC;
OS   Pseudomonas sp. HJ-2.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
```

```
OX   NCBI_TaxID=244327;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HJ-2;
RA   Seo S.H., Choi G.G., Rhee Y.H.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY370931; AAQ72537.1; -.
DR   InterPro; IPR000073; A/b_hydrolase.
DR   InterPro; IPR010941; PhaC_N.
DR   InterPro; IPR010963; PHA_synth_I.
DR   Pfam; PF00561; Abhydrolase_1; 1.
DR   Pfam; PF07167; PhaC_N; 1.
DR   TIGRFAMs; TIGR01838; PHA_synth_I; 1.
SQ   SEQUENCE   566 AA;  63672 MW;  F4CBA7A4CE5943F0 CRC64;

 Q6UFW5  Length: 566  October 13, 2004 13:25  Type: P  Check: 4418  ..
Found using 'claim36' (zara371.key)

           |-------|
1       MDNGHTFAHYWSGQAPFIASFVLQQLRLYVAQNTWFSGHDQSQWFDVPVEALEQLQADYQ
             6       14

61      QQWA

...

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1 match found in sequence:
 q70hx4 ; Hypothetical protein.
  (from "claim36uni.pep")
  TOIG of: q70hx4  check: 6871  from: 1  to: 180

 ID   Q70HX4      PRELIMINARY;      PRT;   180 AA.
 AC   Q70HX4;
 DT   05-JUL-2004 (TrEMBLrel. 27, Created)
 DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE   Hypothetical protein.
 OS   Streptomyces parvulus.
 OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC   Streptomycineae; Streptomycetaceae; Streptomyces.
 OX   NCBI_TaxID=146923;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=Tu4055;
 RX   PubMed=15112998;
 RA   Olano C., Wilkinson B., Sanchez C., Moss S., Sheridan R., Math V.,
 RA   Weston A.J., Brana A.F., Martin C. .J., Oliynyk M., Mendez C.,
 RA   Leadlay P.F., Salas J.A.;
 RT   "Biosynthesis of the angiogenesis inhibitor borrelidin by Streptomyces
 RT   parvulu s Tu4055: cluster analysis and assigment of functions.";
 RL   Chem. Biol. 11:87-97(2004).
 RN   [2]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=Tu4055;
 RA   Olano C., Wilkinson B., Moss S., Brana A.F., Mendez C., Leadlay P.F.,
 RA   Salas J.A.;
 RT   "Evidence from engineered gene fusions for the repeated use of a
 RT   module in a modular polyketide synthase";.";
 RL   Chem. Commun. 22:2780-2782(2003).
 DR   EMBL; AJ580915; CAE45695.1; -.
 DR   InterPro; IPR002048; EF-hand.
 DR   InterPro; IPR010983; EF_Hand_like.
 DR   Pfam; PF00036; efhand; 3.
 DR   SMART; SM00054; EFh; 3.
 DR   PROSITE; PS00018; EF_HAND; 2.
 KW   Calcium; Calcium-binding; Hypothetical protein.
 SQ   SEQUENCE   180 AA;  19338 MW;  6CCE28A1E48436DB CRC64;

 Q70HX4  Length: 180  October 13, 2004 13:25  Type: P  Check: 6871  ..
Found using 'claim36' (zara371.key)

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```
                                                                |-------|
7.      EAAKRVELVFSLFDANGNGVIDSDDFDLMTDRVVAAAAGSDDSAKAAVRAAFRRYWTTLA
                                                               57      65

67      TELDADGDGVITVEEFRPFVLDPERFGPTIAEFARALSALGDPDGDGLI

...

-------
1 match found in sequence:
 q7mgu7 ; Sensor histidine kinase.
  (from "claim36uni.pep")
  TOIG of: q7mgu7  check: 6631  from: 1  to: 1156

 ID   Q7MGU7      PRELIMINARY;      PRT;  1156 AA.
 AC   Q7MGU7;
 DT   01-MAR-2004 (TrEMBLrel. 26, Created)
 DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE   Sensor histidine kinase.
 GN   Name=VV3129;
 OS   Vibrio vulnificus (strain YJ016).
 OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC   Vibrionaceae; Vibrio.
 OX   NCBI_TaxID=196600;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RX   PubMed=14656965;
 RA   Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
 RA   Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
 RA   Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
 RT   "Comparative genome analysis of Vibrio vulnificus, a marine
 RT   pathogen.";
 RL   Genome Res. 13:2577-2587(2003).
 CC   -!- SIMILARITY: Contains 1 histidine kinase domain.
 DR   EMBL; AP005342; BAC95893.1; -.
 DR   GO; GO:0016020; C:membrane; IEA.
 DR   GO; GO:0005524; F:ATP binding; IEA.
 DR   GO; GO:0003677; F:DNA binding; IEA.
 DR   GO; GO:0016301; F:kinase activity; IEA.
 DR   GO; GO:0005215; F:transporter activity; IEA.
 DR   GO; GO:0000156; F:two-component response regulator activity; IEA.
 DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
 DR   GO; GO:0006810; P:transport; IEA.
 DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
 DR   InterPro; IPR003594; ATPbind_ATPase.
 DR   InterPro; IPR004358; Bact_sens_pr_C.
 DR   InterPro; IPR005467; His_kinase.
 DR   InterPro; IPR003661; His_kinA_N.
 DR   InterPro; IPR001734; Na/solut_symport.
 DR   InterPro; IPR001789; Response_reg.
 DR   Pfam; PF02518; HATPase_c; 1.
 DR   Pfam; PF00512; HisKA; 1.
 DR   Pfam; PF00072; Response_reg; 1.
 DR   PRINTS; PR00344; BCTRLSENSOR.
 DR   ProDom; PD000039; Response_reg; 1.
 DR   PROSITE; PS50109; HIS_KIN; 1.
 DR   PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
 DR   PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 KW   Kinase; Phosphorylation; Sensory transduction; Transferase.
 SQ   SEQUENCE   1156 AA;  128283 MW;  4DB3AB41A0B1A4FB CRC64;

 Q7MGU7  Length: 1156  October 13, 2004 13:25  Type: P  Check: 6631  ..
Found using 'claim36' (zara371.key)

...

                                                                |-------|
518     PSLSERLQSASFVGTPLPENENISLYQSRVTVGELEMLASRFVGRNRVKNAFAHYWSQQR
                                                               568     576

578     ETLLPNQQAPSTLIRHTERVLAGVFGASSAKLVLTSALQGRNMQLEEVA
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1 match found in sequence:
 q86p24 ; RE22501p (Fragment).
  (from "claim36uni.pep")
  TOIG of: q86p24  check: 8357  from: 1  to: 972

 ID   Q86P24      PRELIMINARY;      PRT;   972 AA.
 AC   Q86P24;
 DT   01-JUN-2003 (TrEMBLrel. 24, Created)
 DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE   RE22501p (Fragment).
 GN   ORFNames=CG16718;
 OS   Drosophila melanogaster (Fruit fly).
 OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC   Ephydroidea; Drosophilidae; Drosophila.
 OX   NCBI_TaxID=7227;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=Berkeley;
 RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA   Celniker S.;
 RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 DR   EMBL; BT003522; AAO39526.1; -.
 DR   FlyBase; FBgn0038721; CG16718.
 DR   InterPro; IPR007632; DUF590.
 DR   Pfam; PF04547; DUF590; 1.
 FT   NON_TER       1      1
 SQ   SEQUENCE   972 AA;  112363 MW;  57DF924CFD245843 CRC64;

  Q86P24  Length: 972  October 13, 2004 13:25  Type: P  Check: 8357  ..
 Found using 'claim36' (zara371.key)

...

                                                                |-------|
348      VPVKDICQSGNTNITMCPLCDWCNFWDLKETCNYAKVTYLIDNPSTVFFAVFMSFWATLF
                                                              398     406

408      LELWKRYSAEITHRWDLTGFDVHEEHPRPQYLARLEHIPPTRVDYVTNI

...

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1 match found in sequence:
 q8dcz5 ; Signal transduction histidine kinase.
  (from "claim36uni.pep")
  TOIG of: q8dcz5  check: 2146  from: 1  to: 1143

 ID   Q8DCZ5      PRELIMINARY;      PRT;  1143 AA.
 AC   Q8DCZ5;
 DT   01-MAR-2003 (TrEMBLrel. 23, Created)
 DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE   Signal transduction histidine kinase.
 GN   OrderedLocusNames=VV11242;
 OS   Vibrio vulnificus.
 OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC   Vibrionaceae; Vibrio.
 OX   NCBI_TaxID=672;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=CMCP6;
 RA   Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA   Choy H.E.;
 RT   "Complete genome sequence of Vibrio vulnificus CMCP6.";
 RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 CC   -!- SIMILARITY: Contains 1 histidine kinase domain.
 DR   EMBL; AE016801; AAO09698.1; -.
 DR   GO; GO:0016020; C:membrane; IEA.
 DR   GO; GO:0005524; F:ATP binding; IEA.
 DR   GO; GO:0003677; F:DNA binding; IEA.
 DR   GO; GO:0016301; F:kinase activity; IEA.
 DR   GO; GO:0016740; F:transferase activity; IEA.
 DR   GO; GO:0005215; F:transporter activity; IEA.
 DR   GO; GO:0000156; F:two-component response regulator activity; IEA.
 DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
 DR   GO; GO:0007600; P:sensory perception; IEA.
 DR   GO; GO:0006810; P:transport; IEA.
 DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
 DR   InterPro; IPR003594; ATPbind_ATPase.
 DR   InterPro; IPR004358; Bact_sens_pr_C.
 DR   InterPro; IPR011006; CheY_like.
 DR   InterPro; IPR005467; His_kinase.
 DR   InterPro; IPR003661; His_kinA_N.
 DR   InterPro; IPR009082; His_kin_homodim.
 DR   InterPro; IPR001734; Na/solut_symport.
 DR   InterPro; IPR000014; PAS.
 DR   InterPro; IPR001789; Response_reg.
 DR   Pfam; PF02518; HATPase_c; 1.
 DR   Pfam; PF00512; HisKA; 1.
 DR   Pfam; PF00072; Response_reg; 1.
 DR   PRINTS; PR00344; BCTRLSENSOR.
 DR   ProDom; PD000039; Response_reg; 1.
 DR   SMART; SM00387; HATPase_c; 1.
 DR   SMART; SM00388; HisKA; 1.
 DR   SMART; SM00091; PAS; 1.
 DR   SMART; SM00448; REC; 1.
 DR   PROSITE; PS50109; HIS_KIN; 1.
 DR   PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
 DR   PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 KW   Complete proteome; Kinase; Phosphorylation; Sensory transduction;
 KW   Transferase.
 SQ   SEQUENCE   1143 AA;  126643 MW;  85F47E27E3B2D621 CRC64;

  Q8DCZ5  Length: 1143  October 13, 2004 13:25  Type: P  Check: 2146  ..
 Found using 'claim36' (zara371.key)

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                                                                |-------|
505      PSLSERLQSASFVGTPLPENENISLYQSRVTVGELEMLASRFVGRNRVKNAFAHYWSQQR
                                                              555     563

565      ETLLPNQQAPSTLIRHTERVLAGVFGASSAKLVLTSALQGRNMQLEEVA

...

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1 match found in sequence:
 q8in71 ; CG16718-PB.
  (from "claim36uni.pep")
  TOIG of: q8in71  check: 3404  from: 1  to: 926

 ID   Q8IN71      PRELIMINARY;      PRT;   926 AA.
 AC   Q8IN71;
 DT   01-MAR-2003 (TrEMBLrel. 23, Created)
 DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE   CG16718-PB.
 GN   ORFNames=CG16718;
 OS   Drosophila melanogaster (Fruit fly).
 OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC   Ephydroidea; Drosophilidae; Drosophila.
 OX   NCBI_TaxID=7227;
 RN   [1]
 RP   SEQUENCE FROM N.A.
```

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RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FLYBASE;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FLYBASE;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003727; AAN13804.1; -.
DR   FlyBase; FBgn0038721; CG16718.
DR   InterPro; IPR007632; DUF590.
DR   Pfam; PF04547; DUF590; 1.
SQ   SEQUENCE   926 AA;  107585 MW;  1F33F7DDEAE07368 CRC64;

 Q8IN71  Length: 926  October 13, 2004 13:25  Type: P  Check: 3404  ..
Found using 'claim36' (zara371.key)

...

                                                                    |-------|
302     VPVKDICQSGNTNITMCPLCDWCNFWDLKETCNYAKVTYLIDNPSTVFFAVFMSFWATLF
                                                                  352     360

362     LELWKRYSAEITHRWDLTGFDVHEEHPRPQYLARLEHIPPTRVDYVTNI

...

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1 match found in sequence:
 q8lb06 ; Putative glucan endo-1-3-beta-glucosidase.
  (from "claim36uni.pep")
  TOIG of: q8lb06  check: 8289  from: 1  to: 460

 ID   Q8LB06      PRELIMINARY;      PRT;   460 AA.
 AC   Q8LB06;
 DT   01-OCT-2002 (TrEMBLrel. 22, Created)
 DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE   Putative glucan endo-1-3-beta-glucosidase.
 OS   Arabidopsis thaliana (Mouse-ear cress).
 OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX   NCBI_TaxID=3702;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RX   MEDLINE=22088475; PubMed=12093376;
 RA   Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA   Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT   "Full-length messenger RNA sequences greatly improve genome
 RT   annotation.";
 RL   Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 RN   [2]
 RP   SEQUENCE FROM N.A.
 RA   Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA   Feldmann K.;
 RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR   EMBL; AY087496; AAM65039.1; -.
 DR   HSSP; P12257; 1AQ0.
 DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR   InterPro; IPR000490; Glyco_hydro_17.
 DR   Pfam; PF00332; Glyco_hydro_17; 1.
 DR   PROSITE; PS00587; GLYCOSYL_HYDROL_F17; UNKNOWN_1.
 SQ   SEQUENCE   460 AA;  50643 MW;  DF3361006601162C CRC64;

 Q8LB06  Length: 460  October 13, 2004 13:25  Type: P  Check: 8289  ..
Found using 'claim36' (zara371.key)

...

                                                                    |-------|
370     IWCVVAKGANWTQLGDALSYACSQGNNTCDPIQRGGPCQKPDLTVLHASYAFSSYWAQFR
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                                                                420     428

430     KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL

-------
1 match found in sequence:
 q8lby4 ; Beta-1,3-glucanase, putative.
  (from "claim36uni.pep")
  TOIG of: q8lby4  check: 2648  from: 1  to: 476

 ID   Q8LBY4      PRELIMINARY;      PRT;   476 AA.
 AC   Q8LBY4;
 DT   01-OCT-2002 (TrEMBLrel. 22, Created)
 DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE   Beta-1,3-glucanase, putative.
 OS   Arabidopsis thaliana (Mouse-ear cress).
 OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX   NCBI_TaxID=3702;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RX   MEDLINE=22088475; PubMed=12093376;
 RA   Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA   Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT   "Full-length messenger RNA sequences greatly improve genome
 RT   annotation.";
 RL   Genome Biol. 3:RESEARCH0029-RESEARCH0029(2).
 RN   [2]
 RP   SEQUENCE FROM N.A.
 RA   Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA   Feldmann K.;
 RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR   EMBL; AY086926; AAM64490.1; -.
 DR   HSSP; P15737; 1GHS.
 DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR   InterPro; IPR000490; Glyco_hydro_17.
 DR   InterPro; IPR011050; Pectin_lyas_like.
 DR   Pfam; PF00332; Glyco_hydro_17; 1.
 DR   PROSITE; PS00587; GLYCOSYL_HYDROL_F17; UNKNOWN_1.
 SQ   SEQUENCE   476 AA;  52087 MW;  22DDEEA17FA96EB3 CRC64;

  Q8LBY4  Length: 476  October 13, 2004 13:25  Type: P  Check: 2648  ..
 Found using 'claim36' (zara371.key)

...

                                                              |-------|
386     VWCVAVDGADEAELGQALNFACGRSNATCAALAPGGECYAPVTVTWHASYAFSSYWAQFR
                                                            436     444

446     NQSSQCYFNGLARETTTNPGNERCKFPSVTL

-------
1 match found in sequence:
 q9lk41 ; Beta-1,3-glucanase.
  (from "claim36uni.pep")
  TOIG of: q9lk41  check: 2170  from: 1  to: 476

 ID   Q9LK41      PRELIMINARY;      PRT;   476 AA.
 AC   Q9LK41;
 DT   01-OCT-2000 (TrEMBLrel. 15, Created)
 DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE   Beta-1,3-glucanase.
 OS   Arabidopsis thaliana (Mouse-ear cress).
 OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX   NCBI_TaxID=3702;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RX   MEDLINE=20363099; PubMed=10907853;
 RA   Nakamura Y.;
 RT   "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT   Sequence features of the regions of 4,251,695 bp covered by ninety P1,
 RT   TAC and BAC clones.";
 RL   DNA Res. 7:217-221(2000).
 RN   [2]
 RP   SEQUENCE FROM N.A.
 RA   Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 DR   EMBL; AP000377; BAB01853.1; -.
 DR   HSSP; P15737; 1GHS.
 DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR   InterPro; IPR000490; Glyco_hydro_17.
 DR   Pfam; PF00332; Glyco_hydro_17; 1.
 DR   PROSITE; PS00587; GLYCOSYL_HYDROL_F17; UNKNOWN_1.
 SQ   SEQUENCE   476 AA;  52170 MW;  9B36D1BA6109B46E CRC64;

  Q9LK41  Length: 476  October 13, 2004 13:25  Type: P  Check: 2170  ..
 Found using 'claim36' (zara371.key)

...

                                                              |-------|
386     VWCVAVDGADEAELGQALNFACGRSNATCAALAPGGECYAPVTVTWHASYAFSSYWAQFR
                                                            436     444

446     NQSSQCYFNGLARETTTNPGNERCKFPSVTL

-------
1 match found in sequence:
 q9sfw1 ; Putative beta-1,3-glucanase.
  (from "claim36uni.pep")
  TOIG of: q9sfw1  check: 9732  from: 1  to: 440

 ID   Q9SFW1      PRELIMINARY;      PRT;   440 AA.
 AC   Q9SFW1;
 DT   01-MAY-2000 (TrEMBLrel. 13, Created)
 DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE   Putative beta-1,3-glucanase.
 GN   Name=T1B9.1;
 OS   Arabidopsis thaliana (Mouse-ear cress).
 OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX   NCBI_TaxID=3702;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RA   Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
 RA   Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA   Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 DR   EMBL; AC012395; AAF20214.1; -.
 DR   HSSP; P12257; 1AQ0.
 DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR   InterPro; IPR000490; Glyco_hydro_17.
 DR   Pfam; PF00332; Glyco_hydro_17; 1.
 DR   PROSITE; PS00587; GLYCOSYL_HYDROL_F17; UNKNOWN_1.
 SQ   SEQUENCE   440 AA;  48538 MW;  FC8B6A3B3B4B8D93 CRC64;

  Q9SFW1  Length: 440  October 13, 2004 13:25  Type: P  Check: 9732  ..
 Found using 'claim36' (zara371.key)

...

                                                              |-------|
350     KTEYKESLPAPENNDLYKGKIWCVGNNTCDPIQRGGPCQKPDLTVLHASYAFSSYWAQFR
                                                            400     408
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410     KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL

-------
1 match found in sequence:
 q9srt4 ; Putative glucan endo-1-3-beta-glucosidase (Putative beta-1,3-
  (from "claim36uni.pep")
  TOIG of: q9srt4  check: 8766  from: 1  to: 460

 ID   Q9SRT4      PRELIMINARY;      PRT;   460 AA.
 AC   Q9SRT4;
 DT   01-MAY-2000 (TrEMBLrel. 13, Created)
 DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE   Putative glucan endo-1-3-beta-glucosidase (Putative beta-1,3-
 DE   glucanase) (Putative glycosyl hydrolase).
 GN   Name=F21O3.3; Synonyms=At3g07320, At3g07320/T1B9_1;
 OS   Arabidopsis thaliana (Mouse-ear cress).
 OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX   NCBI_TaxID=3702;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RA   Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
 RA   Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA   Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN   [2]
 RP   SEQUENCE FROM N.A.
 RA   Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA   Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
 RA   Hayashizaki Y., Shinozaki K.;
 RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
 RN   [3]
 RP   SEQUENCE FROM N.A.
 RA   Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA   Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
 RA   Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA   Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
 RA   Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
 RA   Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
 RA   Theologis A.;
 RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 DR   EMBL; AC009853; AAF02143.1; -.
 DR   EMBL; AK118068; BAC42699.1; -.
 DR   EMBL; BT005678; AAO64098.1; -.
 DR   HSSP; P12257; 1AQ0.
 DR   GO; GO:0016787; F:hydrolase activity; IEA.
 DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR   InterPro; IPR000490; Glyco_hydro_17.
 DR   Pfam; PF00332; Glyco_hydro_17; 1.
 DR   PROSITE; PS00587; GLYCOSYL_HYDROL_F17; UNKNOWN_1.
 KW   Hydrolase.
 SQ   SEQUENCE   460 AA;  50603 MW;  D2061EAA09C0F85F CRC64;

  Q9SRT4  Length: 460  October 13, 2004 13:25  Type: P  Check: 8766  ..
 Found using 'claim36' (zara371.key)

...

                                                              |-------|
370     IWCVVAKGANWTQLGDALSYACSQGNNTCDPIQRGGPCQKPDLTVLHASYAFSSYWAQFR
                                                            420     428

430     KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL

-------
1 match found in sequence:
 q9vdv4 ; CG16718-PA (LD10322p).
  (from "claim36uni.pep")
  TOIG of: q9vdv4  check: 1097  from: 1  to: 1075

ID   Q9VDV4      PRELIMINARY;      PRT;  1075 AA.
AC   Q9VDV4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CG16718-PA (LD10322p).
GN   ORFNames=CG16718;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
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RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FLYBASE;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FLYBASE;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003727; AAF55685.1; -.
DR   EMBL; BT010299; AAQ23617.1; -.
DR   IntAct; Q9VDV4; -.
DR   FlyBase; FBgn0038721; CG16718.
DR   InterPro; IPR007632; DUF590.
DR   Pfam; PF04547; DUF590; 1.
SQ   SEQUENCE   1075 AA;  123934 MW;  729765FBD8339C70 CRC64;

 Q9VDV4  Length: 1075  October 13, 2004 13:25  Type: P  Check: 1097  ..
Found using 'claim36' (zara371.key)

...

                                                              |-------|
451     VPVKDICQSGNTNITMCPLCDWCNFWDLKETCNYAKVTYLIDNPSTVFFAVFMSFWATLF
                                                            501     509

511     LELWKRYSAEITHRWDLTGFDVHEEHPRPQYLARLEHIPPTRVDYVTNI

...


                      -- Search Statistics --

Times:                    CPU                  Total Elapsed
                      00:00:00.00              00:00:00.00

Number of sequences searched:                      17
Number of sequence hits:                           17
Number of separate matches:                        17
Number of sequence hits saved:                      0
```

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> O <
O|  |O  IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

                -- Outline of search "claim36_spt" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "zara371.key":
  claim36 (AA) ID   claim36 AA preliminary pattern
1       followed by
2         r or n or a or t or v
2         f
2         m or i or t or r or a or s
2         r or h or e or c or s or d
2         h or f or y
2         w
2         e or t or a or f or s
2         g or q or t or a or d
2         f or q or l

Selected files:

        File : claim36spt.pep

                    -- Output Parameters --

Format Options:                       File Options:
  Nucleic acid code matching   Exact     Indirect file              No
  Find non-matching hits only  No        Sequence or key file       No
  Report key used              Yes       List of hits               Yes
  Note position of hit         Yes       Hit display                Yes
  Display full annotations     Yes       Name and annotations       Yes
  Sequence context             50


                        -- Run Parameters --

  Run mode                     Batch
    Time to start comparison   now
    Notify at end of run       No

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1 match found in sequence:
 p72824 ; Hypothetical protein sll1200.
  (from "claim36spt.pep")
  TOIG of: p72824  check: 9387  from: 1  to: 391

 ID   P72824      PRELIMINARY;      PRT;   391 AA.
 AC   P72824;
 DT   01-FEB-1997 (TrEMBLrel. 02, Created)
 DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE   Hypothetical protein sll1200.
 GN   SLL1200.
 OS   Synechocystis sp. (strain PCC 6803).
 OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX   NCBI_TaxID=1148;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RX   MEDLINE=97061201; PubMed=8905231;
 RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
 RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA   Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA   Tabata S.;
 RT   "Sequence analysis of the genome of the unicellular cyanobacterium
 RT   Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT   entire genome and assignment of potential protein-coding regions.";
 RL   DNA Res. 3:109-136(1996).
 DR   EMBL; D90901; BAA16839.1; -.
 DR   PIR; S74688; S74688.
 DR   InterPro; IPR007110; Ig-like.
 KW   Hypothetical protein; Complete proteome.
 SQ   SEQUENCE   391 AA;  42240 MW;  1AFDB350FDED2A45 CRC64;

  P72824  Length: 391  October 13, 2004 13:38  Type: P  Check: 9387  ..
 Found using 'claim36' (zara371.key)

...

                                                                |-------|
296      FWLPAIAFSWLLGSSILNNGLIPLLLEILQGNQTGVGIGLYFGCVGLAGDVFTRYWSTQS
                                                              346     354

356      SQMHGGLGLAMLVMSTLLCARYWQGFRVPNKKGAGD

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1 match found in sequence:
 q06913 ; Beta-1,3-glucanase homologue (Fragment).
  (from "claim36spt.pep")
  TOIG of: q06913  check: 219  from: 1  to: 139

 ID   Q06913      PRELIMINARY;      PRT;   139 AA.
 AC   Q06913;
 DT   01-NOV-1996 (TrEMBLrel. 01, Created)
 DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE   Beta-1,3-glucanase homologue (Fragment).
 OS   Brassica napus (Rape).
 OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC   eurosids II; Brassicales; Brassicaceae; Brassica.
 OX   NCBI_TaxID=3708;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RX   MEDLINE=94108487; PubMed=8281185;
 RA   Hird D.L., Worrall D., Hodge R., Smartt S., Paul W., Scott R.;
 RT   "The anther-specific protein encoded by the Brassica napus and
 RT   Arabidopsis thaliana A6 gene displays similarity to beta-1,3-
 RT   glucanases.";
 RL   Plant J. 4:1023-1033(1993).
 DR   EMBL; X69889; CAA49515.1; -.
 DR   PIR; S31612; S31612.
 DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR   InterPro; IPR000490; Glyco_hydro_17.
 DR   Pfam; PF00332; Glyco_hydro_17; 1.
 FT   NON_TER       1       1
 SQ   SEQUENCE   139 AA;  14995 MW;  ECBBD63335C551F7 CRC64;

   Q06913  Length: 139  October 13, 2004 13:38  Type: P  Check: 219  ..
 Found using 'claim36' (zara371.key)

...

                                                            |-------|
49       VWCVAVEGANETELGQALDFACGRSNATCAALAPGRECYAPVSVTWHASYAFSSYWAQFR
                                                          99      107

109      NQSSQCYFNGLARETTTNPGNEQCKFPSVTL

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1 match found in sequence:
 q86p24 ; RE22501p (Fragment).
  (from "claim36spt.pep")
  TOIG of: q86p24  check: 8357  from: 1  to: 972

 ID   Q86P24      PRELIMINARY;      PRT;   972 AA.
 AC   Q86P24;
 DT   01-JUN-2003 (TrEMBLrel. 24, Created)
 DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
```

ILC 10/22

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DE   RE22501p (Fragment).
GN   CG16718.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=y;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT003522; AAO39526.1; -.
DR   InterPro; IPR007632; DUF590.
DR   Pfam; PF04547; DUF590; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   972 AA;  112363 MW;  57DF924CFD245843 CRC64;

 Q86P24  Length: 972  October 13, 2004 13:38  Type: P  Check: 8357  ..
Found using 'claim36' (zara371.key)

...

                                                        |-------|
348      VPVKDICQSGNTNITMCPLCDWCNFWDLKETCNYAKVTYLIDNPSTVFFAVFMSFWATLF
                                                      398     406

408      LELWKRYSAEITHRWDLTGFDVHEEHPRPQYLARLEHIPPTRVDYVTNI

...

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1 match found in sequence:
 q8dcz5 ; Signal transduction histidine kinase.
  (from "claim36spt.pep")
  TOIG of: q8dcz5  check: 2146  from: 1  to: 1143

 ID   Q8DCZ5      PRELIMINARY;      PRT;  1143 AA.
 AC   Q8DCZ5;
 DT   01-MAR-2003 (TrEMBLrel. 23, Created)
 DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE   Signal transduction histidine kinase.
 GN   VV11242.
 OS   Vibrio vulnificus.
 OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC   Vibrionaceae; Vibrio.
 OX   NCBI_TaxID=672;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=CMCP6;
 RA   Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA   Choy H.E.;
 RT   "Complete genome sequence of Vibrio vulnificus CMCP6.";
 RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 DR   EMBL; AE016801; AAO09698.1; -.
 DR   GO; GO:0016020; C:membrane; IEA.
 DR   GO; GO:0005524; F:ATP binding; IEA.
 DR   GO; GO:0003677; F:DNA binding; IEA.
 DR   GO; GO:0016301; F:kinase activity; IEA.
 DR   GO; GO:0005215; F:transporter activity; IEA.
 DR   GO; GO:0000156; F:two-component response regulator activity; IEA.
 DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
 DR   GO; GO:0006810; P:transport; IEA.
 DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
 DR   InterPro; IPR003594; ATPbind_ATPase.
 DR   InterPro; IPR004358; Bact_sens_pr_C.
 DR   InterPro; IPR005467; His_kinase.
 DR   InterPro; IPR003661; His_kinA_N.
 DR   InterPro; IPR001734; Na/solut_symport.
 DR   InterPro; IPR001789; Response_reg.
 DR   Pfam; PF02518; HATPase_c; 1.
 DR   Pfam; PF00512; HisKA; 1.
 DR   Pfam; PF00072; response_reg; 1.
 DR   PRINTS; PR00344; BCTRLSENSOR.
 DR   ProDom; PD000039; Response_reg; 1.
 DR   SMART; SM00387; HATPase_c; 1.
 DR   SMART; SM00388; HisKA; 1.
 DR   SMART; SM00448; REC; 1.
 DR   PROSITE; PS50109; HIS_KIN; 1.
 DR   PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
 DR   PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 KW   Kinase; Complete proteome.
 SQ   SEQUENCE   1143 AA;  126643 MW;  85F47E27E3B2D621 CRC64;

  Q8DCZ5  Length: 1143  October 13, 2004 13:38  Type: P  Check: 2146  ..
 Found using 'claim36' (zara371.key)

...

                                                                |-------|
505      PSLSERLQSASFVGTPLPENENISLYQSRVTVGELEMLASRFVGRNRVKNAFAHYWSQQR
                                                               555     563

565      ETLLPNQQAPSTLIRHTERVLAGVFGASSAKLVLTSALQGRNMQLEEVA

...

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1 match found in sequence:
 q8in71 ; CG16718-PB.
  (from "claim36spt.pep")
  TOIG of: q8in71  check: 3404  from: 1  to: 926

 ID   Q8IN71      PRELIMINARY;      PRT;  926 AA.
 AC   Q8IN71;
 DT   01-MAR-2003 (TrEMBLrel. 23, Created)
 DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE   CG16718-PB.
 GN   CG16718.
 OS   Drosophila melanogaster (Fruit fly).
 OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC   Ephydroidea; Drosophilidae; Drosophila.
 OX   NCBI_TaxID=7227;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RX   MEDLINE=20196006; PubMed=10731132;
 RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA   Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA   Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA   Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA   Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA   Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA   Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA   Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA   McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA   Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA   Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA   Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA   Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT   "Sequencing of Drosophila melanogaster genome.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA   Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA   Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA   Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA   Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA   Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA   Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT   "Annotation of Drosophila melanogaster genome.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003727; AAN13804.1; -.
DR   FlyBase; FBgn0038721; CG16718.
DR   InterPro; IPR007632; DUF590.
DR   Pfam; PF04547; DUF590; 1.
SQ   SEQUENCE   926 AA;  107585 MW;  1F33F7DDEAE07368 CRC64;

 Q8IN71  Length: 926  October 13, 2004 13:38  Type: P  Check: 3404  ..
Found using 'claim36' (zara371.key)

...

                                                                |-------|
302      VPVKDICQSGNTNITMCPLCDWCNFWDLKETCNYAKVTYLIDNPSTVFFAVFMSFWATLF
                                                              352     360

362      LELWKRYSAEITHRWDLTGFDVHEEHPRPQYLARLEHIPPTRVDYVTNI

...

-------
1 match found in sequence:
q8lb06 ; Putative glucan endo-1-3-beta-glucosidase.
 (from "claim36spt.pep")
 TOIG of: q8lb06  check: 8289  from: 1  to: 460

ID   Q8LB06      PRELIMINARY;      PRT;   460 AA.
AC   Q8LB06;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Putative glucan endo-1-3-beta-glucosidase.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA   Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT   "Full-length messenger RNA sequences greatly improve genome
RT   annotation.";
RL   Genome Biol. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA   Feldmann K.;
RT   "Full-Length cDNA from Arabidopsis thaliana.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY087496; AAM65039.1; -.
DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   InterPro; IPR000490; Glyco_hydro_17.
DR   Pfam; PF00332; Glyco_hydro_17; 1.
DR   PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
SQ   SEQUENCE   460 AA;  50643 MW;  DF3361006601162C CRC64;

 Q8LB06  Length: 460  October 13, 2004 13:38  Type: P  Check: 8289  ..
Found using 'claim36' (zara371.key)

...

                                                                |-------|
370      IWCVVAKGANWTQLGDALSYACSQGNNTCDPIQRGGPCQKPDLTVLHASYAFSSYWAQFR
                                                              420     428

430      KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL

-------
1 match found in sequence:
q8lby4 ; Beta-1,3-glucanase, putative.
 (from "claim36spt.pep")
 TOIG of: q8lby4  check: 2648  from: 1  to: 476

ID   Q8LBY4      PRELIMINARY;      PRT;   476 AA.
AC   Q8LBY4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-1,3-glucanase, putative.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA   Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT   "Full-length messenger RNA sequences greatly improve genome
RT   annotation.";
RL   Genome Biol. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
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RA   Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA   Feldmann K.;
RT   "Full-Length cDNA from Arabidopsis thaliana.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY086926; AAM64490.1; -.
DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   InterPro; IPR000490; Glyco_hydro_17.
DR   Pfam; PF00332; Glyco_hydro_17; 1.
DR   PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
SQ   SEQUENCE   476 AA;  52087 MW;  22DDEEA17FA96EB3 CRC64;

 Q8LBY4  Length: 476  October 13, 2004 13:38  Type: P  Check: 2648  ..
Found using 'claim36' (zara371.key)

...

                                                              |-------|
386     VWCVAVDGADEAELGQALNFACGRSNATCAALAPGGECYAPVTVTWHASYAFSSYWAQFR
                                                            436     444

446     NQSSQCYFNGLARETTTNPGNERCKFPSVTL

-------
1 match found in sequence:
 q9lk41 ; Beta-1,3-glucanase.
  (from "claim36spt.pep")
  TOIG of: q9lk41  check: 2170  from: 1  to: 476

 ID   Q9LK41      PRELIMINARY;      PRT;   476 AA.
 AC   Q9LK41;
 DT   01-OCT-2000 (TrEMBLrel. 15, Created)
 DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE   Beta-1,3-glucanase.
 OS   Arabidopsis thaliana (Mouse-ear cress).
 OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX   NCBI_TaxID=3702;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=Columbia;
 RA   Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 RN   [2]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=Columbia;
 RX   MEDLINE=20363099; PubMed=10907853;
 RA   Nakamura Y.;
 RT   "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT   Sequence features of the regions of 4,251,695 bp covered by ninety P1,
 RT   TAC and BAC clones.";
 RL   DNA Res. 7:217-221(2000).
 DR   EMBL; AP000377; BAB01853.1; -.
 DR   HSSP; P15737; 1GHS.
 DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR   InterPro; IPR000490; Glyco_hydro_17.
 DR   Pfam; PF00332; Glyco_hydro_17; 1.
 DR   PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
 SQ   SEQUENCE   476 AA;  52170 MW;  9B36D1BA6109B46E CRC64;

  Q9LK41  Length: 476  October 13, 2004 13:38  Type: P  Check: 2170  ..
 Found using 'claim36' (zara371.key)

 ...

                                                               |-------|
 386     VWCVAVDGADEAELGQALNFACGRSNATCAALAPGGECYAPVTVTWHASYAFSSYWAQFR
                                                             436     444

 446     NQSSQCYFNGLARETTTNPGNERCKFPSVTL

 -------
 1 match found in sequence:
  q9sfw1 ; Putative beta-1,3-glucanase.
   (from "claim36spt.pep")
   TOIG of: q9sfw1  check: 9732  from: 1  to: 440

  ID   Q9SFW1      PRELIMINARY;      PRT;   440 AA.
  AC   Q9SFW1;
  DT   01-MAY-2000 (TrEMBLrel. 13, Created)
  DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
  DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
  DE   Putative beta-1,3-glucanase.
  GN   T1B9.1.
  OS   Arabidopsis thaliana (Mouse-ear cress).
  OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
  OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  OX   NCBI_TaxID=3702;
  RN   [1]
  RP   SEQUENCE FROM N.A.
  RC   STRAIN=cv. Columbia;
  RA   Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
  RA   Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
  RA   Bowman C.L., White O., Nierman W.C., Fraser C.M.;
  RT   "Arabidopsis thaliana chromosome III BAC T1B9 genomic sequence.";
  RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
  DR   EMBL; AC012395; AAF20214.1; -.
  DR   HSSP; P12257; 1AQ0.
  DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
  DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
  DR   InterPro; IPR000490; Glyco_hydro_17.
  DR   Pfam; PF00332; Glyco_hydro_17; 1.
  DR   PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
  SQ   SEQUENCE   440 AA;  48538 MW;  FC8B6A3B3B4B8D93 CRC64;

   Q9SFW1  Length: 440  October 13, 2004 13:38  Type: P  Check: 9732  ..
  Found using 'claim36' (zara371.key)

  ...

                                                                |-------|
 350     KTEYKESLPAPENNDLYKGKIWCVGNNTCDPIQRGGPCQKPDLTVLHASYAFSSYWAQFR
                                                               400     408

 410     KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL

 -------
 1 match found in sequence:
  q9srt4 ; Putative glucan endo-1-3-beta-glucosidase (Putative beta-1,3-glucanas
   (from "claim36spt.pep")
   TOIG of: q9srt4  check: 8766  from: 1  to: 460

  ID   Q9SRT4      PRELIMINARY;      PRT;   460 AA.
  AC   Q9SRT4;
  DT   01-MAY-2000 (TrEMBLrel. 13, Created)
  DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
  DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
  DE   Putative glucan endo-1-3-beta-glucosidase (Putative beta-1,3-glucanase
  DE   precursor) (Putative glycosyl hydrolase).
  GN   F21O3.3 OR AT3G07320/T1B9_1 OR AT3G07320.
  OS   Arabidopsis thaliana (Mouse-ear cress).
  OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
  OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  OX   NCBI_TaxID=3702;
  RN   [1]
  RP   SEQUENCE FROM N.A.
  RC   STRAIN=cv. Columbia;
  RA   Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
  RA   Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
  RA   Bowman C.L., White O., Nierman W.C., Fraser C.M.;
  RT   "Arabidopsis thaliana chromosome III BAC F21O3 genomic sequence.";
```

```
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RA   Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA   Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA   Hayashizaki Y., Shinozaki K.;
RT   "Arabidopsis thaliana full-length cDNA.";
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA   Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA   Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA   Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA   Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA   Theologis A.;
RT   "Arabidopsis Open Reading Frame (ORF) Clones.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC009853; AAF02143.1; -.
DR   EMBL; AK118068; BAC42699.1; -.
DR   EMBL; BT005678; AAO64098.1; -.
DR   HSSP; P12257; 1AQ0.
DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   InterPro; IPR000490; Glyco_hydro_17.
DR   Pfam; PF00332; Glyco_hydro_17; 1.
DR   PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
KW   Hydrolase.
SQ   SEQUENCE   460 AA;  50603 MW;  D2061EAA09C0F85F CRC64;

 Q9SRT4  Length: 460  October 13, 2004 13:38  Type: P  Check: 8766  ..
Found using 'claim36' (zara371.key)

...

                                                              |-------|
370      IWCVVAKGANWTQLGDALSYACSQGNNTCDPIQRGGPCQKPDLTVLHASYAFSSYWAQFR
                                                            420     428

430      KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL

-------
1 match found in sequence:
 q9vdv4 ; CG16718 protein.
  (from "claim36spt.pep")
  TOIG of: q9vdv4  check: 1097  from: 1  to: 1075

 ID   Q9VDV4      PRELIMINARY;      PRT;  1075 AA.
 AC   Q9VDV4;
 DT   01-MAY-2000 (TrEMBLrel. 13, Created)
 DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE   CG16718 protein.
 GN   CG16718.
 OS   Drosophila melanogaster (Fruit fly).
 OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC   Ephydroidea; Drosophilidae; Drosophila.
 OX   NCBI_TaxID=7227;
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=Berkeley;
 RX   MEDLINE=20196006; PubMed=10731132;
 RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT   "The genome sequence of Drosophila melanogaster.";
 RL   Science 287:2185-2195(2000).
 DR   EMBL; AE003727; AAF55685.1; -.
 DR   FlyBase; FBgn0038721; CG16718.
 DR   InterPro; IPR007632; DUF590.
 DR   Pfam; PF04547; DUF590; 1.
 SQ   SEQUENCE   1075 AA;  123934 MW;  729765FBD8339C70 CRC64;

  Q9VDV4  Length: 1075  October 13, 2004 13:38  Type: P  Check: 1097  ..
 Found using 'claim36' (zara371.key)

 ...

                                                              |-------|
 451      VPVKDICQSGNTNITMCPLCDWCNFWDLKETCNYAKVTYLIDNPSTVFFAVFMSFWATLF
                                                            501     509

 511      LELWKRYSAEITHRWDLTGFDVHEEHPRPQYLARLEHIPPTRVDYVTNI

 ...


                        -- Search Statistics --

 Times:                      CPU                  Total Elapsed
                        00:00:00.00              00:00:00.00

 Number of sequences searched:                        11
 Number of sequence hits:                             11
 Number of separate matches:                          11
 Number of sequence hits saved:                        0
```

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> O <
O|  |O  IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

              -- Outline of search "claim36_pir" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "zara371.key":
  claim36 (AA) ID   claim36 AA preliminary pattern
1       followed by
2         r or n or a or t or v
2         f
2         m or i or t or r or a or s
2         r or h or e or c or s or d
2         h or f or y
2         w
2         e or t or a or f or s
2         g or q or t or a or d
2         f or q or l

Selected files:

        File : claim36pir.pep

                    -- Output Parameters --

Format Options:                        File Options:
  Nucleic acid code matching   Exact      Indirect file              No
  Find non-matching hits only  No         Sequence or key file       No
  Report key used              Yes        List of hits               Yes
  Note position of hit         Yes        Hit display                Yes
  Display full annotations     Yes        Name and annotations       Yes
  Sequence context             50

                    -- Run Parameters --

  Run mode                     Batch
    Time to start comparison   now
    Notify at end of run       No

-------
1 match found in sequence:
 s31612 ; TOIG of: s31612  check: 219  from: 1  to: 139
  (from "claim36pir.pep")
  TOIG of: s31612  check: 219  from: 1  to: 139

 F1;S31612 - beta-1,3-glucanase homolog (clone A20) - rape (fragment)
 C;Species: Brassica napus (rape)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Nov-2000
 C;Accession: S31612
 R;Hird, D.; Worrall, D.; Hodge, R.; Paul, W.; Smartt, S.; Draper, J.; Scott, R.
 submitted to the EMBL Data Library, December 1992
 A;Description: The anther-specific protein encoded by the Brassica napus and
  Arabidopsis thaliana A6 gene exhibits homology to beta-1,3-glucanases.
 A;Reference number: S31612
 A;Accession: S31612
 A;Molecule type: mRNA
 A;Residues: 1-139 <HIR>
 A;Cross-references: EMBL:X69889; NID:g17733; PID:g17734
 A;Experimental source: clone A20
 C;Superfamily: beta-1,3-glucanase

   S31612  Length: 139  October 13, 2004 13:40  Type: P  Check: 219  ..
 Found using 'claim36' (zara371.key)

...

                                                          |-------|
```

```
49      VWCVAVEGANETELGQALDFACGRSNATCAALAPGRECYAPVSVTWHASYAFSSYWAQFR
                                                                99      107

109     NQSSQCYFNGLARETTTNPGNEQCKFPSVTL

-------
1 match found in sequence:
 s74688 ; TOIG of: s74688  check: 9387  from: 1  to: 391
  (from "claim36pir.pep")
  TOIG of: s74688  check: 9387  from: 1  to: 391

 P1;S74688 - hypothetical protein sll1200 - Synechocystis sp. (strain PCC 6803)
 C;Species: Synechocystis sp.
 A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C;Accession: S74688
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.;
  Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi,
  T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.;
  Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium
  Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and
  assignment of potential protein-coding regions.
 A;Reference number: S74322; MUID:97061201; PMID:8905231
 A;Accession: S74688
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-391 <KAN>
 A;Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA16839.1;
  PID:d1017572; PID:g1651913
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June
  1996

   S74688  Length: 391  October 13, 2004 13:40  Type: P  Check: 9387  ..
 Found using 'claim36' (zara371.key)

...

                                                          |-------|
296     FWLPAIAFSWLLGSSILNNGLIPLLLEILQGNQTGVGIGLYFGCVGLAGDVFTRYWSTQS
                                                        346     354

356     SQMHGGLGLAMLVMSTLLCARYWQGFRVPNKKGAGD

                    -- Search Statistics --

Times:                    CPU                  Total Elapsed
                      00:00:00.00              00:00:00.00

Number of sequences searched:                      2
Number of sequence hits:                           2
Number of separate matches:                        2
Number of sequence hits saved:                     0
```

102A.

! FINDPATTERNS on Swiss-Prot:* allowing 0 mismatches

! 1 (R,N,A,T,V)F(M,I,T,R,A,S)(R,H,E,C,S,D)(H,F,Y)W(E,T,A,F,S)(G,Q,T,A,D)(F,Q,L)

Databases searched:
SWISS-PROT, Release 42.7, Released on 15Dec2003, Formatted on 15Dec2003

Total finds:	0
Total length:	52,070,155
Total sequences:	141,681
CPU time:	03:00.75

```
> O <
O|  |O  IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

                -- Outline of search "claim36_ags" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "zara371.key":
  claim36 (AA) ID   claim36 AA preliminary pattern
1       followed by
2         r or n or a or t or v
2         f
2         m or i or t or r or a or s
2         r or h or e or c or s or d
2         h or f or y
2         w
2         e or t or a or f or s
2         g or q or t or a or d
2         f or q or l

Selected files:

        File : claim36ags.pep

                    -- Output Parameters --

Format Options:                      File Options:
  Nucleic acid code matching  Exact    Indirect file              No
  Find non-matching hits only No       Sequence or key file       No
  Report key used             Yes      List of hits               Yes
  Note position of hit        Yes      Hit display                Yes
  Display full annotations    Yes      Name and annotations       Yes
  Sequence context            50

                        -- Run Parameters --

  Run mode                    Batch
    Time to start comparison  now
    Notify at end of run      No

-------
1 match found in sequence:
 aab17079 ; Mdm/hdm antagonist peptide sequence SEQ ID NO:135.
  (from "claim36ags.pep")
  TOIG of: aab17079  check: 5978  from: 1  to: 12

 ID   AAB17079 standard; peptide; 12 AA.
 XX
 AC   AAB17079;
 XX
 DT   31-OCT-2000  (first entry)
 XX
 DE   Mdm/hdm antagonist peptide sequence SEQ ID NO:135.
 XX
 KW   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW   immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW   inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW   vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW   thrombosis; pharmaceutical.
 XX
 OS   Synthetic.
 XX
 PN   WO200024782-A2.
 XX
 PD   04-MAY-2000.
 XX
 PF   25-OCT-1999;   99WO-US025044.
 XX
 PR   23-OCT-1998;   98US-0105371P.
 PR   22-OCT-1999;   99US-00428082.
 XX
 PA   (AMGE-) AMGEN INC.
 XX
 PI   Feige U,  Liu C,  Cheetham J,  Boone TC;
 XX
 DR   WPI; 2000-350702/30.
 XX
 PT   Novel composition of matter comprising an Fc domain and pharmacologically
 PT   active peptides, useful for treating cancer and autoimmune diseases.
 XX
 PS   Claim 39; Page 241; 608pp; English.
 XX
 CC   The present invention describes composition of matter (I) comprising an
 CC   Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC   (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC   independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
 CC   (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
 CC   P3, and P4 = are each independently sequences of pharmacologically active
 CC   peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC   c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC   of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC   thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC   cells from the present invention can be used for producing pharmaceutical
 CC   compositions. The compositions are useful for treating cancer, asthma,
 CC   thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC   a Fab domain) can provide a longer half-life or incorporate functions
 CC   such as Fc receptor binding, protein A binding, complement fixation, and
 CC   possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
 CC   AAB18003 represent nucleotide and amino acid sequences used in the
 CC   exemplification of the present invention
 XX
 SQ   Sequence 12 AA;

  AAB17079  Length: 12  October 13, 2004 13:39  Type: P  Check: 5978  ..
 Found using 'claim36' (zara371.key)

          |-------|
1       MPRFMDYWEGLN
          3       11

-------
1 match found in sequence:
 aab17080 ; Mdm/hdm antagonist peptide sequence SEQ ID NO:136.
  (from "claim36ags.pep")
  TOIG of: aab17080  check: 6151  from: 1  to: 12

 ID   AAB17080 standard; peptide; 12 AA.
 XX
 AC   AAB17080;
 XX
 DT   31-OCT-2000  (first entry)
 XX
 DE   Mdm/hdm antagonist peptide sequence SEQ ID NO:136.
 XX
 KW   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW   immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW   inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW   vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW   thrombosis; pharmaceutical.
 XX
 OS   Synthetic.
 XX
 PN   WO200024782-A2.
 XX
 PD   04-MAY-2000.
 XX
 PF   25-OCT-1999;   99WO-US025044.
```

XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Claim 39; Page 242; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 12 AA;

AAB17080 Length: 12 October 13, 2004 13:39 Type: P Check: 6151 ..
Found using 'claim36' (zara371.key)

```
          |-------|
1       VQNFIDYWTQQF
          3       11
```

---
1 match found in sequence:
aab17081 ; Mdm/hdm antagonist peptide sequence SEQ ID NO:137.
(from "claim36ags.pep")
TOIG of: aab17081 check: 5993 from: 1 to: 12

ID AAB17081 standard; peptide; 12 AA.
XX
AC AAB17081;
XX
DT 31-OCT-2000 (first entry)
XX
DE Mdm/hdm antagonist peptide sequence SEQ ID NO:137.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Claim 39; Page 242; 608pp; English.
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CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 12 AA;

AAB17081 Length: 12 October 13, 2004 13:39 Type: P Check: 5993 ..
Found using 'claim36' (zara371.key)

```
          |-------|
1       TGPAFTHYWATF
          4       12
```

---
1 match found in sequence:
aab17082 ; Mdm/hdm antagonist peptide sequence SEQ ID NO:138.
(from "claim36ags.pep")
TOIG of: aab17082 check: 9093 from: 1 to: 15

ID AAB17082 standard; peptide; 15 AA.
XX
AC AAB17082;
XX
DT 31-OCT-2000 (first entry)
XX
DE Mdm/hdm antagonist peptide sequence SEQ ID NO:138.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.

PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Claim 39; Page 242; 608pp; English.
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CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 15 AA;

AAB17082 Length: 15 October 13, 2004 13:39 Type: P Check: 9093 ..
Found using 'claim36' (zara371.key)

```
            |-------|
1       IDRAPTFRDHWFALV
            6       14
```

---
1 match found in sequence:
aab17083 ; Mdm/hdm antagonist peptide sequence SEQ ID NO:139.
(from "claim36ags.pep")
TOIG of: aab17083 check: 9428 from: 1 to: 15

ID AAB17083 standard; peptide; 15 AA.
XX
AC AAB17083;
XX
DT 31-OCT-2000 (first entry)
XX
DE Mdm/hdm antagonist peptide sequence SEQ ID NO:139.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Claim 39; Page 243; 608pp; English.
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CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
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CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 15 AA;

AAB17083 Length: 15 October 13, 2004 13:39 Type: P Check: 9428 ..
Found using 'claim36' (zara371.key)

```
            |-------|
1       PRPALVFADYWETLY
            6       14
```

---
1 match found in sequence:
aab17084 ; Mdm/hdm antagonist peptide sequence SEQ ID NO:140.
(from "claim36ags.pep")
TOIG of: aab17084 check: 8833 from: 1 to: 15

ID AAB17084 standard; peptide; 15 AA.
XX
AC AAB17084;
XX
DT 31-OCT-2000 (first entry)
XX
DE Mdm/hdm antagonist peptide sequence SEQ ID NO:140.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX

PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
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CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 15 AA;

AAB17084 Length: 15 October 13, 2004 13:39 Type: P Check: 8833 ..
Found using 'claim36' (zara371.key)

```
        |-------|
1       PAFSRFWSDLSAGAH
        2       10
```

---
1 match found in sequence:
aag07078 ; Arabidopsis thaliana protein fragment SEQ ID NO: 4092.
(from "claim36ags.pep")
TOIG of: aag07078 check: 9327 from: 1 to: 493

ID AAG07078 standard; protein; 493 AA.
XX
AC AAG07078;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4092.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
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XX
PA   (CERE-) CERES INC.
XX
PI   Alexandrov N,  Brover V,  Chen X,  Subramanian G,  Troukhan ME;
PI   Zheng L,  Dumas J;
XX
DR   WPI; 2000-507395/46.
DR   N-PSDB; AAC33724.
XX
PT   New sequence determined DNA fragments (SDFs) from different plant
PT   species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT   protein coding sequences, untranslated regions, or as 3' termination
PT   sequences.
XX
PS   Claim 19; SEQ ID NO 4092; 344pp + Sequence Listing; English.
XX
CC   The present sequence is a putative protein fragment from Arabidopsis
CC   thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC   of the mRNA obtained from the plant, and creating a cDNA library which
CC   could then be sequenced, allowing the putative protein sequence(s) to be
CC   obtained. This sequence may be useful for protein identification and for
CC   aiding in the elucidation of signal transduction and metabolic pathways.
CC   Its coding sequence has a use in the control of gene expression as a
CC   promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC   the behaviour of a gene within the chromosome, as a tool for use in
CC   genetic mapping, including a use in hybridisation assays, for recognition
CC   or isolation of similar DNA fragments, or for the identification of a
CC   particular organism
XX
SQ   Sequence 493 AA;

 AAG07078  Length: 493  October 13, 2004 13:39  Type: P  Check: 9327  ..
 Found using 'claim36' (zara371.key)

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463      KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL

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1 match found in sequence:
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PA (CERE-) CERES INC.
XX
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
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DR WPI; 2000-507395/46.
DR N-PSDB; AAC33724.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences.
XX
PS Claim 19; SEQ ID NO 4093; 344pp + Sequence Listing; English.
XX
CC The present sequence is a putative protein fragment from Arabidopsis
CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC of the mRNA obtained from the plant, and creating a cDNA library which
CC could then be sequenced, allowing the putative protein sequence(s) to be
CC obtained. This sequence may be useful for protein identification and for
CC aiding in the elucidation of signal transduction and metabolic pathways.
CC Its coding sequence has a use in the control of gene expression as a
CC promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC the behaviour of a gene within the chromosome, as a tool for use in
CC genetic mapping, including a use in hybridisation assays, for recognition
CC or isolation of similar DNA fragments, or for the identification of a
CC particular organism
XX
SQ Sequence 460 AA;

AAG07079 Length: 460 October 13, 2004 13:39 Type: P Check: 8289 ..
Found using 'claim36' (zara371.key)

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430     KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL
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1 match found in sequence:
aag07080 ; Arabidopsis thaliana protein fragment SEQ ID NO: 4094.
(from "claim36ags.pep")
TOIG of: aag07080 check: 563 from: 1 to: 384

ID AAG07080 standard; protein; 384 AA.
XX
AC AAG07080;
XX
DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 4094.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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DR   N-PSDB; AAC33724.
XX
PT   New sequence determined DNA fragments (SDFs) from different plant
PT   species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT   protein coding sequences, untranslated regions, or as 3' termination
PT   sequences.
XX
PS   Claim 19; SEQ ID NO 4094; 344pp + Sequence Listing; English.
XX
CC   The present sequence is a putative protein fragment from Arabidopsis
CC   thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC   of the mRNA obtained from the plant, and creating a cDNA library which
CC   could then be sequenced, allowing the putative protein sequence(s) to be
CC   obtained. This sequence may be useful for protein identification and for
CC   aiding in the elucidation of signal transduction and metabolic pathways.
CC   Its coding sequence has a use in the control of gene expression as a
CC   promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC   the behaviour of a gene within the chromosome, as a tool for use in
CC   genetic mapping, including a use in hybridisation assays, for recognition
CC   or isolation of similar DNA fragments, or for the identification of a
CC   particular organism
XX
SQ   Sequence 384 AA;

 AAG07080  Length: 384  October 13, 2004 13:39  Type: P  Check: 563  ..
Found using 'claim36' (zara371.key)

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354      KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL

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1 match found in sequence:
 aag08312 ; Arabidopsis thaliana protein fragment SEQ ID NO: 5798.

 (from "claim36ags.pep")
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ID   AAG08312 standard; protein; 496 AA.
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XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 5798.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
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XX
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XX
PA   (CERE-) CERES INC.
XX
PI   Alexandrov N,  Brover V,  Chen X,  Subramanian G,  Troukhan ME;
PI   Zheng L,  Dumas J;
XX
DR   WPI; 2000-507395/46.
DR   N-PSDB; AAC34196.
XX
PT   New sequence determined DNA fragments (SDFs) from different plant
PT   species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT   protein coding sequences, untranslated regions, or as 3' termination
PT   sequences.
XX
PS   Claim 19; SEQ ID NO 5798; 344pp + Sequence Listing; English.
XX
CC   The present sequence is a putative protein fragment from Arabidopsis
CC   thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC   of the mRNA obtained from the plant, and creating a cDNA library which
CC   could then be sequenced, allowing the putative protein sequence(s) to be
CC   obtained. This sequence may be useful for protein identification and for
CC   aiding in the elucidation of signal transduction and metabolic pathways.
CC   Its coding sequence has a use in the control of gene expression as a
CC   promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC   the behaviour of a gene within the chromosome, as a tool for use in
CC   genetic mapping, including a use in hybridisation assays, for recognition
CC   or isolation of similar DNA fragments, or for the identification of a
CC   particular organism
XX
SQ   Sequence 496 AA;

AAG08312  Length: 496  October 13, 2004 13:39  Type: P  Check: 8013  ..
Found using 'claim36' (zara371.key)

...

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466      NQSSQCYFNGLARETTTNPGNERCKFPSVTL

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 DE   Arabidopsis thaliana protein fragment SEQ ID NO: 5799.
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 KW   Protein identification; signal transduction pathway; metabolic pathway;
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XX
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XX
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XX
PA   (CERE-) CERES INC.
XX
PI   Alexandrov N,  Brover V,  Chen X,  Subramanian G,  Troukhan ME;
PI   Zheng L,  Dumas J;
XX
DR   WPI; 2000-507395/46.
DR   N-PSDB; AAC34196.
XX
PT   New sequence determined DNA fragments (SDFs) from different plant
PT   species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT   protein coding sequences, untranslated regions, or as 3' termination
PT   sequences.
XX
PS   Claim 19; SEQ ID NO 5799; 344pp + Sequence Listing; English.
XX
CC   The present sequence is a putative protein fragment from Arabidopsis
CC   thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC   of the mRNA obtained from the plant, and creating a cDNA library which
CC   could then be sequenced, allowing the putative protein sequence(s) to be
CC   obtained. This sequence may be useful for protein identification and for
CC   aiding in the elucidation of signal transduction and metabolic pathways.
CC   Its coding sequence has a use in the control of gene expression as a
CC   promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC   the behaviour of a gene within the chromosome, as a tool for use in
CC   genetic mapping, including a use in hybridisation assays, for recognition
CC   or isolation of similar DNA fragments, or for the identification of a
CC   particular organism
XX
SQ   Sequence 476 AA;

AAG08313  Length: 476  October 13, 2004 13:39  Type: P  Check: 2648  ..
Found using 'claim36' (zara371.key)

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446      NQSSQCYFNGLARETTTNPGNERCKFPSVTL

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1 match found in sequence:
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 DT   17-OCT-2000  (first entry)
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 KW   Protein identification; signal transduction pathway; metabolic pathway;
 KW   hybridisation assay; genetic mapping; gene expression control; promoter;
 KW   termination sequence.
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 OS   Arabidopsis thaliana.
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 PD   06-SEP-2000.
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XX
PA   (CERE-) CERES INC.
XX
PI   Alexandrov N,  Brover V,  Chen X,  Subramanian G,  Troukhan ME;
PI   Zheng L,  Dumas J;
XX
DR   WPI; 2000-507395/46.
DR   N-PSDB; AAC34196.
XX
PT   New sequence determined DNA fragments (SDFs) from different plant
PT   species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT   protein coding sequences, untranslated regions, or as 3' termination
PT   sequences.
XX
PS   Claim 19; SEQ ID NO 5800; 344pp + Sequence Listing; English.
XX
CC   The present sequence is a putative protein fragment from Arabidopsis
CC   thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC   of the mRNA obtained from the plant, and creating a cDNA library which
CC   could then be sequenced, allowing the putative protein sequence(s) to be
CC   obtained. This sequence may be useful for protein identification and for
CC   aiding in the elucidation of signal transduction and metabolic pathways.
CC   Its coding sequence has a use in the control of gene expression as a
CC   promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC   the behaviour of a gene within the chromosome, as a tool for use in
CC   genetic mapping, including a use in hybridisation assays, for recognition
CC   or isolation of similar DNA fragments, or for the identification of a
CC   particular organism
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SQ   Sequence 388 AA;

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Found using 'claim36' (zara371.key)

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  (from "claim36ags.pep")
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 XX
 DE   Arabidopsis thaliana protein fragment SEQ ID NO: 48177.
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 KW   Protein identification; signal transduction pathway; metabolic pathway;
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 KW   termination sequence.
 XX
 OS   Arabidopsis thaliana.
 XX
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XX
PA (CERE-) CERES INC.
XX
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
DR WPI; 2000-507395/46.
DR N-PSDB; AAC45900.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences.
XX
PS Claim 19; SEQ ID NO 48177; 344pp + Sequence Listing; English.
XX
CC The present sequence is a putative protein fragment from Arabidopsis
CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC of the mRNA obtained from the plant, and creating a cDNA library which
CC could then be sequenced, allowing the putative protein sequence(s) to be
CC obtained. This sequence may be useful for protein identification and for
CC aiding in the elucidation of signal transduction and metabolic pathways.
CC Its coding sequence has a use in the control of gene expression as a
CC promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC the behaviour of a gene within the chromosome, as a tool for use in
CC genetic mapping, including a use in hybridisation assays, for recognition
CC or isolation of similar DNA fragments, or for the identification of a
CC particular organism

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Found using 'claim36' (zara371.key)

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 KW   Protein identification; signal transduction pathway; metabolic pathway;
 KW   hybridisation assay; genetic mapping; gene expression control; promoter;
 KW   termination sequence.
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PA   (CERE-) CERES INC.
XX
PI   Alexandrov N,  Brover V,  Chen X,  Subramanian G,  Troukhan ME;
PI   Zheng L,  Dumas J;
XX
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DR   N-PSDB; AAC45900.
XX
PT   New sequence determined DNA fragments (SDFs) from different plant
PT   species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT   protein coding sequences, untranslated regions, or as 3' termination
PT   sequences.
XX
PS   Claim 19; SEQ ID NO 48178; 344pp + Sequence Listing; English.
XX
CC   The present sequence is a putative protein fragment from Arabidopsis
CC   thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC   of the mRNA obtained from the plant, and creating a cDNA library which
CC   could then be sequenced, allowing the putative protein sequence(s) to be
CC   obtained. This sequence may be useful for protein identification and for
CC   aiding in the elucidation of signal transduction and metabolic pathways.
CC   Its coding sequence has a use in the control of gene expression as a
CC   promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC   the behaviour of a gene within the chromosome, as a tool for use in
CC   genetic mapping, including a use in hybridisation assays, for recognition
CC   or isolation of similar DNA fragments, or for the identification of a
CC   particular organism
XX
SQ   Sequence 460 AA;

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 Found using 'claim36' (zara371.key)

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430      KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL
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XX
PA (CERE-) CERES INC.
XX
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
DR WPI; 2000-507395/46.
DR N-PSDB; AAC45900.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species; e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences.
XX
PS Claim 19; SEQ ID NO 48179; 344pp + Sequence Listing; English.
XX
CC The present sequence is a putative protein fragment from Arabidopsis
CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC of the mRNA obtained from the plant, and creating a cDNA library which
CC could then be sequenced, allowing the putative protein sequence(s) to be
CC obtained. This sequence may be useful for protein identification and for
CC aiding in the elucidation of signal transduction and metabolic pathways.
CC Its coding sequence has a use in the control of gene expression as a
CC promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC the behaviour of a gene within the chromosome, as a tool for use in
CC genetic mapping, including a use in hybridisation assays, for recognition
CC or isolation of similar DNA fragments, or for the identification of a
CC particular organism
XX
SQ Sequence 384 AA;

AAG38989 Length: 384 October 13, 2004 13:39 Type: P Check: 1002 ..
Found using 'claim36' (zara371.key)

...

294 IWCVVAKGANWTQLGDALSYACSQGNNTCDPIQRGGPCQKPDLTVLHASYAFSSYWAQFR
344 352

354 KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL

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1 match found in sequence:
aag52473 ; Arabidopsis thaliana protein fragment SEQ ID NO: 66706.
(from "claim36ags.pep")
TOIG of: aag52473 check: 8156 from: 1 to: 496

ID AAG52473 standard; protein; 496 AA.
XX
AC AAG52473;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66706.
XX

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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PA   (CERE-) CERES INC.
XX
PI   Alexandrov N,  Brover V,  Chen X,  Subramanian G,  Troukhan ME;
PI   Zheng L,  Dumas J;
XX
DR   WPI; 2000-507395/46.
DR   N-PSDB; AAC50943.
XX
PT   New sequence determined DNA fragments (SDFs) from different plant
PT   species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT   protein coding sequences, untranslated regions, or as 3' termination
PT   sequences.
XX
PS   Claim 19; SEQ ID NO 66706; 344pp + Sequence Listing; English.
XX
CC   The present sequence is a putative protein fragment from Arabidopsis
CC   thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC   of the mRNA obtained from the plant, and creating a cDNA library which
CC   could then be sequenced, allowing the putative protein sequence(s) to be
CC   obtained. This sequence may be useful for protein identification and for
CC   aiding in the elucidation of signal transduction and metabolic pathways.
CC   Its coding sequence has a use in the control of gene expression as a
CC   promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC   the behaviour of a gene within the chromosome, as a tool for use in
CC   genetic mapping, including a use in hybridisation assays, for recognition
CC   or isolation of similar DNA fragments, or for the identification of a
CC   particular organism
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SQ   Sequence 496 AA;

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XX
PA (CERE-) CERES INC.
XX
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
DR WPI; 2000-507395/46.
DR N-PSDB; AAC50943.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences.
XX
PS Claim 19; SEQ ID NO 66707; 344pp + Sequence Listing; English.
XX
CC The present sequence is a putative protein fragment from Arabidopsis
CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC of the mRNA obtained from the plant, and creating a cDNA library which
CC could then be sequenced, allowing the putative protein sequence(s) to be
CC obtained. This sequence may be useful for protein identification and for
CC aiding in the elucidation of signal transduction and metabolic pathways.
CC Its coding sequence has a use in the control of gene expression as a
CC promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC the behaviour of a gene within the chromosome, as a tool for use in
CC genetic mapping, including a use in hybridisation assays, for recognition
CC or isolation of similar DNA fragments, or for the identification of a
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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
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PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
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PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
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PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
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PR 22-JUL-1999; 99US-0145192P.
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PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
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PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
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PR 08-OCT-1999; 99US-0158232P.
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PR 21-OCT-1999; 99US-0160767P.
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PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
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PR 08-NOV-1999; 99US-0164150P.
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PR 10-NOV-1999; 99US-0164545P.
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PR 12-NOV-1999; 99US-0164962P.
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PR 18-NOV-1999; 99US-0166157P.
PR 18-NOV-1999; 99US-0166158P.
PR 18-NOV-1999; 99US-0166173P.
PR 19-NOV-1999; 99US-0166411P.
PR 19-NOV-1999; 99US-0166412P.
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PR 22-NOV-1999; 99US-0166750P.
PR 23-NOV-1999; 99US-0167362P.
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PR 24-NOV-1999; 99US-0167234P.
PR 24-NOV-1999; 99US-0167235P.
PR 24-NOV-1999; 99US-0167382P.
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PR 30-NOV-1999; 99US-0167904P.
PR 30-NOV-1999; 99US-0167908P.
PR 01-DEC-1999; 99US-0168231P.
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PR 02-DEC-1999; 99US-0168546P.
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PR 03-DEC-1999; 99US-0168675P.
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PR 07-DEC-1999; 99US-0169298P.
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PR 08-DEC-1999; 99US-0169692P.
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PR 16-DEC-1999; 99US-0171107P.
PR 16-DEC-1999; 99US-0171114P.
PR 19-JAN-2000; 2000US-0176866P.
PR 19-JAN-2000; 2000US-0176867P.
PR 19-JAN-2000; 2000US-0176910P.
PR 26-JAN-2000; 2000US-0178166P.
PR 27-JAN-2000; 2000US-0177666P.
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PR 28-JAN-2000; 2000US-0178754P.
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PR 01-FEB-2000; 2000US-0179388P.
PR 01-FEB-2000; 2000US-0179395P.
PR 03-FEB-2000; 2000US-0180039P.
PR 03-FEB-2000; 2000US-0180139P.
PR 04-FEB-2000; 2000US-0180206P.
PR 04-FEB-2000; 2000US-0180207P.
PR 07-FEB-2000; 2000US-0180695P.
PR 07-FEB-2000; 2000US-0180696P.
PR 09-FEB-2000; 2000US-0181214P.
PR 09-FEB-2000; 2000US-0181228P.
PR 10-FEB-2000; 2000US-0181476P.
PR 10-FEB-2000; 2000US-0181551P.
PR 15-FEB-2000; 2000US-0182477P.
PR 15-FEB-2000; 2000US-0182478P.
PR 15-FEB-2000; 2000US-0182512P.
PR 15-FEB-2000; 2000US-0182516P.
PR 17-FEB-2000; 2000US-0183165P.
PR 17-FEB-2000; 2000US-0183166P.
XX
PA (CERE-) CERES INC.
XX
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
DR WPI; 2000-507395/46.
DR N-PSDB; AAC50943.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences.
XX
PS Claim 19; SEQ ID NO 66708; 344pp + Sequence Listing; English.
XX
CC The present sequence is a putative protein fragment from Arabidopsis
CC thaliana. Its coding sequence was isolated by carrying out RT-PCR on all
CC of the mRNA obtained from the plant, and creating a cDNA library which
CC could then be sequenced, allowing the putative protein sequence(s) to be
CC obtained. This sequence may be useful for protein identification and for
CC aiding in the elucidation of signal transduction and metabolic pathways.
CC Its coding sequence has a use in the control of gene expression as a
CC promoter, coding sequence, 3'UTR or termination sequence, for controlling
CC the behaviour of a gene within the chromosome, as a tool for use in

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CC   genetic mapping, including a use in hybridisation assays, for recognition
CC   or isolation of similar DNA fragments, or for the identification of a
CC   particular organism
XX
SQ   Sequence 388 AA;

AAG52475  Length: 388  October 13, 2004 13:39  Type: P  Check: 1903  ..
Found using 'claim36' (zara371.key)

...

                                                          |-------|
298      VWCVAVDGADEAELGQALNFACGRSNATCAALAPGGECYAPVTVTWHASYAFSSYWAQFR
                                                        348     356

358      NQSSQCYFNGLARETTTNPGNERCKFPSVTL

-------
1 match found in sequence:
 aaw37170 ; Human oncogenic protein MDM2 binding peptide 1.
  (from "claim36ags.pep")
 TOIG of: aaw37170  check: 5978  from: 1  to: 12

 ID   AAW37170 standard; peptide; 12 AA.
 XX
 AC   AAW37170;
 XX
 DT   20-JUL-1998  (first entry)
 XX
 DE   Human oncogenic protein MDM2 binding peptide 1.
 XX
 KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW   tumour; diagnosis; binding; viral infection.
 XX
 OS   Synthetic.
 OS   Homo sapiens.
 XX
 PN   WO9801467-A2.
 XX
 PD   15-JAN-1998.
 XX
 PF   04-JUL-1997;   97WO-EP003549.
 XX
 PR   05-JUL-1996;   96GB-00014197.
 PR   07-APR-1997;   97GB-00007041.
 XX
 PA   (NOVS ) NOVARTIS AG.
 PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
 PI   Garcia-Echeverria C,  Chene P,  Furet P;
 XX
 DR   WPI; 1998-100996/09.
 XX
 PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT   and identifying binding agents.
 XX
 PS   Claim 5; Page 41; 45pp; English.
 XX
 CC   This peptide is capable of binding to an oncogenic protein MDM2
 CC   (especially human DM2). The MDM2 binding peptides can specifically
 CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
 CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
 CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
 CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
 CC   molecules that bind to MDM2 and to identify and design inhibitors of
 CC   MDM2/p53 binding. They may also be used to purify binding partners
 CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
 CC   cancer and leukaemia patients and for treatment or prevention of disease
 CC   involving p53/MDM2 interactions, especially tumours and viral infections.
 CC   The peptides can be administered nasally, rectally, orally or by
 CC   injection. By interfering with MDM2/p53 interaction, the peptides can
 CC   activate p53 function and accumulation in normal cells. The peptides
 CC   which mimic the MDM2 binding site in p53, have a significantly greater
 CC   blocking activity compared with wild-type p53
 XX
 SQ   Sequence 12 AA;

  AAW37170  Length: 12  October 13, 2004 13:39  Type: P  Check: 5978  ..
 Found using 'claim36' (zara371.key)

          |-------|
1       MPRFMDYWEGLN
          3       11

-------
1 match found in sequence:
 aaw37172 ; Human oncogenic protein MDM2 binding peptide 3.
  (from "claim36ags.pep")
  TOIG of: aaw37172  check: 9428  from: 1  to: 15

 ID   AAW37172 standard; peptide; 15 AA.
 XX
 AC   AAW37172;
 XX
 DT   20-JUL-1998  (first entry)
 XX
 DE   Human oncogenic protein MDM2 binding peptide 3.
 XX
 KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW   tumour; diagnosis; binding; viral infection.
 XX
 OS   Synthetic.
 OS   Homo sapiens.
 XX
 PN   WO9801467-A2.
 XX
 PD   15-JAN-1998.
 XX
 PF   04-JUL-1997;   97WO-EP003549.
 XX
 PR   05-JUL-1996;   96GB-00014197.
 PR   07-APR-1997;   97GB-00007041.
 XX
 PA   (NOVS ) NOVARTIS AG.
 PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
 PI   Garcia-Echeverria C,  Chene P,  Furet P;
 XX
 DR   WPI; 1998-100996/09.
 XX
 PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT   and identifying binding agents.
 XX
 PS   Disclosure; Page 4; 45pp; English.
 XX
 CC   This peptide is capable of binding to an oncogenic protein MDM2
 CC   (especially human DM2). The MDM2 binding peptides can specifically
 CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
 CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
 CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
 CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
 CC   molecules that bind to MDM2 and to identify and design inhibitors of
 CC   MDM2/p53 binding. They may also be used to purify binding partners
 CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
 CC   cancer and leukaemia patients and for treatment or prevention of disease
 CC   involving p53/MDM2 interactions, especially tumours and viral infections.
 CC   The peptides can be administered nasally, rectally, orally or by
 CC   injection. By interfering with MDM2/p53 interaction, the peptides can
 CC   activate p53 function and accumulation in normal cells. The peptides
 CC   which mimic the MDM2 binding site in p53, have a significantly greater
 CC   blocking activity compared with wild-type p53
 XX
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SQ   Sequence 15 AA;

 AAW37172  Length: 15  October 13, 2004 13:39  Type: P  Check: 9428  ..
Found using 'claim36' (zara371.key)

            |-------|
1       PRPALVFADYWETLY
            6       14

-------
1 match found in sequence:
 aaw37179 ; Human oncogenic protein MDM2 binding peptide derivative 7.
  (from "claim36ags.pep")
  TOIG of: aaw37179  check: 3427  from: 1  to: 9

 ID   AAW37179 standard; peptide; 9 AA.
 XX
 AC   AAW37179;
 XX
 DT   20-JUL-1998  (first entry)
 XX
 DE   Human oncogenic protein MDM2 binding peptide derivative 7.
 XX
 KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW   tumour; diagnosis; binding; viral infection.
 XX
 OS   Synthetic.
 OS   Homo sapiens.
 XX
 PN   WO9801467-A2.
 XX
 PD   15-JAN-1998.
 XX
 PF   04-JUL-1997;   97WO-EP003549.
 XX
 PR   05-JUL-1996;   96GB-00014197.
 PR   07-APR-1997;   97GB-00007041.
 XX
 PA   (NOVS ) NOVARTIS AG.
 PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
 PI   Garcia-Echeverria C,  Chene P,  Furet P;
 XX
 DR   WPI; 1998-100996/09.
 XX
 PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT   and identifying binding agents.
 XX
 PS   Disclosure; Page 8; 45pp; English.
 XX
 CC   This peptide is capable of binding to an oncogenic protein MDM2
 CC   (especially human DM2). The MDM2 binding peptides can specifically
 CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
 CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
 CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
 CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
 CC   molecules that bind to MDM2 and to identify and design inhibitors of
 CC   MDM2/p53 binding. They may also be used to purify binding partners
 CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
 CC   cancer and leukaemia patients and for treatment or prevention of disease
 CC   involving p53/MDM2 interactions, especially tumours and viral infections.
 CC   The peptides can be administered nasally, rectally, orally or by
 CC   injection. By interfering with MDM2/p53 interaction, the peptides can
 CC   activate p53 function and accumulation in normal cells. The peptides
 CC   which mimic the MDM2 binding site in p53, have a significantly greater
 CC   blocking activity compared with wild-type p53
 XX
 SQ   Sequence 9 AA;

  AAW37179  Length: 9  October 13, 2004 13:39  Type: P  Check: 3427  ..
Found using 'claim36' (zara371.key)

            |-------|
1       RFMDYWEGL
            1       9

-------
1 match found in sequence:
 aaw37182 ; Human oncogenic protein MDM2 binding N-acylated peptide derivative
  (from "claim36ags.pep")
  TOIG of: aaw37182  check: 5993  from: 1  to: 12

 ID   AAW37182 standard; peptide; 12 AA.
 XX
 AC   AAW37182;
 XX
 DT   20-JUL-1998  (first entry)
 XX
 DE   Human oncogenic protein MDM2 binding N-acylated peptide derivative 1.
 XX
 KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW   tumour; diagnosis; binding; viral infection.
 XX
 OS   Synthetic.
 OS   Homo sapiens.
 XX
 FH   Key             Location/Qualifiers
 FT   Modified-site   1
 FT                   /note= "N-terminal acetyl"
 FT   Modified-site   12
 FT                   /note= "C-terminal amide"
 XX
 PN   WO9801467-A2.
 XX
 PD   15-JAN-1998.
 XX
 PF   04-JUL-1997;   97WO-EP003549.
 XX
 PR   05-JUL-1996;   96GB-00014197.
 PR   07-APR-1997;   97GB-00007041.
 XX
 PA   (NOVS ) NOVARTIS AG.
 PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
 PI   Garcia-Echeverria C,  Chene P,  Furet P;
 XX
 DR   WPI; 1998-100996/09.
 XX
 PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT   and identifying binding agents.
 XX
 PS   Example 1; Page 18; 45pp; English.
 XX
 CC   This is a N-acylated peptide derivative capable of binding to a human
 CC   oncogenic protein MDM2. The MDM2 binding peptides can specifically
 CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
 CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
 CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
 CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
 CC   molecules that bind to MDM2 and to identify and design inhibitors of
 CC   MDM2/p53 binding. They may also be used to purify binding partners
 CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
 CC   cancer and leukaemia patients and for treatment or prevention of disease
 CC   involving p53/MDM2 interactions, especially tumours and viral infections.
 CC   The peptides can be administered nasally, rectally, orally or by
 CC   injection. By interfering with MDM2/p53 interaction, the peptides can
 CC   activate p53 function and accumulation in normal cells. The peptides
 CC   which mimic the MDM2 binding site in p53, have a significantly greater
 CC   blocking activity compared with wild-type p53
 XX
 SQ   Sequence 12 AA;
```

```
 AAW37182  Length: 12  October 13, 2004 13:39  Type: P  Check: 5993  ..
Found using 'claim36' (zara371.key)

          |-------|
1       TGPAFTHYWATF
           4       12

-------
1 match found in sequence:
aaw37183 ; Human oncogenic protein MDM2 binding N-acylated peptide derivative
 (from "claim36ags.pep")
 TOIG of: aaw37183  check: 5978  from: 1  to: 12

ID   AAW37183 standard; peptide; 12 AA.
XX
AC   AAW37183;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human oncogenic protein MDM2 binding N-acylated peptide derivative 2.
XX
KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW   tumour; diagnosis; binding; viral infection.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal acetyl"
FT   Modified-site   12
FT                   /note= "C-terminal amide"
XX
PN   WO9801467-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-EP003549.
XX
PR   05-JUL-1996;   96GB-00014197.
PR   07-APR-1997;   97GB-00007041.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
PI   Garcia-Echeverria C,  Chene P,  Furet P;
XX
DR   WPI; 1998-100996/09.
XX
PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
PT   and identifying binding agents.
XX
PS   Example 1; Page 19; 45pp; English.
XX
CC   This is a N-acylated peptide derivative capable of binding to a human
CC   oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC   molecules that bind to MDM2 and to identify and design inhibitors of
CC   MDM2/p53 binding. They may also be used to purify binding partners
CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
CC   cancer and leukaemia patients and for treatment or prevention of disease
CC   involving p53/MDM2 interactions, especially tumours and viral infections.
CC   The peptides can be administered nasally, rectally, orally or by
CC   injection. By interfering with MDM2/p53 interaction, the peptides can
CC   activate p53 function and accumulation in normal cells. The peptides
CC   which mimic the MDM2 binding site in p53, have a significantly greater
CC   blocking activity compared with wild-type p53
XX
SQ   Sequence 12 AA;

 AAW37183  Length: 12  October 13, 2004 13:39  Type: P  Check: 5978  ..
Found using 'claim36' (zara371.key)

          |-------|
1       MPRFMDYWEGLN
           3       11

-------
1 match found in sequence:
aaw37191 ; Human oncogenic protein MDM2 binding N-acylated peptide derivative
 (from "claim36ags.pep")
 TOIG of: aaw37191  check: 6151  from: 1  to: 12

ID   AAW37191 standard; peptide; 12 AA.
XX
AC   AAW37191;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human oncogenic protein MDM2 binding N-acylated peptide derivative 10.
XX
KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW   tumour; diagnosis; binding; viral infection.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal acetyl"
FT   Modified-site   12
FT                   /note= "C-terminal amide"
XX
PN   WO9801467-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-EP003549.
XX
PR   05-JUL-1996;   96GB-00014197.
PR   07-APR-1997;   97GB-00007041.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
PI   Garcia-Echeverria C,  Chene P,  Furet P;
XX
DR   WPI; 1998-100996/09.
XX
PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
PT   and identifying binding agents.
XX
PS   Example 1; Page 19; 45pp; English.
XX
CC   This is a N-acylated peptide derivative capable of binding to a human
CC   oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC   molecules that bind to MDM2 and to identify and design inhibitors of
CC   MDM2/p53 binding. They may also be used to purify binding partners
CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
CC   cancer and leukaemia patients and for treatment or prevention of disease
CC   involving p53/MDM2 interactions, especially tumours and viral infections.
CC   The peptides can be administered nasally, rectally, orally or by
CC   injection. By interfering with MDM2/p53 interaction, the peptides can
CC   activate p53 function and accumulation in normal cells. The peptides
CC   which mimic the MDM2 binding site in p53, have a significantly greater
```

```
CC   blocking activity compared with wild-type p53
XX
SQ   Sequence 12 AA;

 AAW37191  Length: 12  October 13, 2004 13:39  Type: P  Check: 6151  ..
Found using 'claim36' (zara371.key)

          |-------|
1       VQNFIDYWTQQF
          3       11

-------
1 match found in sequence:
 aaw37192 ; Human oncogenic protein MDM2 binding N-acylated peptide derivative
  (from "claim36ags.pep")
  TOIG of: aaw37192  check: 9093  from: 1  to: 15

ID   AAW37192 standard; peptide; 15 AA.
XX
AC   AAW37192;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human oncogenic protein MDM2 binding N-acylated peptide derivative 11.
XX
KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW   tumour; diagnosis; binding; viral infection.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal acetyl"
FT   Modified-site   15
FT                   /note= "C-terminal amide"
XX
PN   WO9801467-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-EP003549.
XX
PR   05-JUL-1996;   96GB-00014197.
PR   07-APR-1997;   97GB-00007041.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
PI   Garcia-Echeverria C,  Chene P,  Furet P;
XX
DR   WPI; 1998-100996/09.
XX
PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
PT   and identifying binding agents.
XX
PS   Example 1; Page 19; 45pp; English.
XX
CC   This is a N-acylated peptide derivative capable of binding to a human
CC   oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC   molecules that bind to MDM2 and to identify and design inhibitors of
CC   MDM2/p53 binding. They may also be used to purify binding partners
CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
CC   cancer and leukaemia patients and for treatment or prevention of disease
CC   involving p53/MDM2 interactions, especially tumours and viral infections.
CC   The peptides can be administered nasally, rectally, orally or by
CC   injection. By interfering with MDM2/p53 interaction, the peptides can
CC   activate p53 function and accumulation in normal cells. The peptides
CC   which mimic the MDM2 binding site in p53, have a significantly greater
CC   blocking activity compared with wild-type p53
XX
SQ   Sequence 15 AA;

 AAW37192  Length: 15  October 13, 2004 13:39  Type: P  Check: 9093  ..
Found using 'claim36' (zara371.key)

             |-------|
1         IDRAPTFRDHWFALV
             6       14

-------
1 match found in sequence:
 aaw37193 ; Human oncogenic protein MDM2 binding N-acylated peptide derivative
  (from "claim36ags.pep")
  TOIG of: aaw37193  check: 9428  from: 1  to: 15

ID   AAW37193 standard; peptide; 15 AA.
XX
AC   AAW37193;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human oncogenic protein MDM2 binding N-acylated peptide derivative 12.
XX
KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW   tumour; diagnosis; binding; viral infection.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal acetyl"
FT   Modified-site   15
FT                   /note= "C-terminal amide"
XX
PN   WO9801467-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-EP003549.
XX
PR   05-JUL-1996;   96GB-00014197.
PR   07-APR-1997;   97GB-00007041.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
PI   Garcia-Echeverria C,  Chene P,  Furet P;
XX
DR   WPI; 1998-100996/09.
XX
PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
PT   and identifying binding agents.
XX
PS   Example 1; Page 19; 45pp; English.
XX
CC   This is a N-acylated peptide derivative capable of binding to a human
CC   oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC   molecules that bind to MDM2 and to identify and design inhibitors of
CC   MDM2/p53 binding. They may also be used to purify binding partners
CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
CC   cancer and leukaemia patients and for treatment or prevention of disease
CC   involving p53/MDM2 interactions, especially tumours and viral infections.
```

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CC   The peptides can be administered nasally, rectally, orally or by
CC   injection. By interfering with MDM2/p53 interaction, the peptides can
CC   activate p53 function and accumulation in normal cells. The peptides
CC   which mimic the MDM2 binding site in p53, have a significantly greater
CC   blocking activity compared with wild-type p53
XX
SQ   Sequence 15 AA;

 AAW37193  Length: 15  October 13, 2004 13:39  Type: P  Check: 9428  ..
Found using 'claim36' (zara371.key)

            |-------|
1       PRPALVFADYWETLY
            6       14

-------
1 match found in sequence:
aaw37194 ; Human oncogenic protein MDM2 binding N-acylated peptide derivative
 (from "claim36ags.pep")
 TOIG of: aaw37194  check: 8833  from: 1  to: 15

ID   AAW37194 standard; peptide; 15 AA.
XX
AC   AAW37194;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human oncogenic protein MDM2 binding N-acylated peptide derivative 13.
XX
KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW   tumour; diagnosis; binding; viral infection.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal acetyl"
FT   Modified-site   15
FT                   /note= "C-terminal amide"
XX
PN   WO9801467-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-EP003549.
XX
PR   05-JUL-1996;   96GB-00014197.
PR   07-APR-1997;   97GB-00007041.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
PI   Garcia-Echeverria C,  Chene P,  Furet P;
XX
DR   WPI; 1998-100996/09.
XX
PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
PT   and identifying binding agents.
XX
PS   Example 1; Page 19; 45pp; English.
XX
CC   This is a N-acylated peptide derivative capable of binding to a human
CC   oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC   molecules that bind to MDM2 and to identify and design inhibitors of
CC   MDM2/p53 binding. They may also be used to purify binding partners
CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
CC   cancer and leukaemia patients and for treatment or prevention of disease
CC   involving p53/MDM2 interactions, especially tumours and viral infections.
CC   The peptides can be administered nasally, rectally, orally or by
CC   injection. By interfering with MDM2/p53 interaction, the peptides can
CC   activate p53 function and accumulation in normal cells. The peptides
CC   which mimic the MDM2 binding site in p53, have a significantly greater
CC   blocking activity compared with wild-type p53
XX
SQ   Sequence 15 AA;

 AAW37194  Length: 15  October 13, 2004 13:39  Type: P  Check: 8833  ..
Found using 'claim36' (zara371.key)

            |-------|
1       PAFSRFWSDLSAGAH
            2       10

-------
1 match found in sequence:
aaw37195 ; Human oncogenic protein MDM2 binding C-amidated peptide derivative
 (from "claim36ags.pep")
 TOIG of: aaw37195  check: 5993  from: 1  to: 12

ID   AAW37195 standard; peptide; 12 AA.
XX
AC   AAW37195;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human oncogenic protein MDM2 binding C-amidated peptide derivative 1.
XX
KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW   tumour; diagnosis; binding; viral infection.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   12
FT                   /note= "C-terminal amide"
XX
PN   WO9801467-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-EP003549.
XX
PR   05-JUL-1996;   96GB-00014197.
PR   07-APR-1997;   97GB-00007041.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
PI   Garcia-Echeverria C,  Chene P,  Furet P;
XX
DR   WPI; 1998-100996/09.
XX
PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
PT   and identifying binding agents.
XX
PS   Example 1; Page 20; 45pp; English.
XX
CC   This is a C-amidated peptide derivative capable of binding to a human
CC   oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC   molecules that bind to MDM2 and to identify and design inhibitors of
CC   MDM2/p53 binding. They may also be used to purify binding partners
CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
```

CC cancer and leukaemia patients and for treatment or prevention of disease
CC involving p53/MDM2 interactions, especially tumours and viral infections.
CC The peptides can be administered nasally, rectally, orally or by
CC injection. By interfering with MDM2/p53 interaction, the peptides can
CC activate p53 function and accumulation in normal cells. The peptides
CC which mimic the MDM2 binding site in p53, have a significantly greater
CC blocking activity compared with wild-type p53
XX
SQ Sequence 12 AA;

AAW37195 Length: 12 October 13, 2004 13:39 Type: P Check: 5993 ..
Found using 'claim36' (zara371.key)

```
          |-------|
1       TGPAFTHYWATF
           4       12
```

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1 match found in sequence:
aaw37196 ; Human oncogenic protein MDM2 binding C-amidated peptide derivative
(from "claim36ags.pep")
TOIG of: aaw37196 check: 5978 from: 1 to: 12

ID AAW37196 standard; peptide; 12 AA.
XX
AC AAW37196;
XX
DT 20-JUL-1998 (first entry)
XX
DE Human oncogenic protein MDM2 binding C-amidated peptide derivative 2.
XX
KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW tumour; diagnosis; binding; viral infection.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 12
FT /note= "C-terminal amide"
XX
PN WO9801467-A2.
XX
PD 15-JAN-1998.
XX
PF 04-JUL-1997; 97WO-EP003549.
XX
PR 05-JUL-1996; 96GB-00014197.
PR 07-APR-1997; 97GB-00007041.
XX
PA (NOVS) NOVARTIS AG.
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
PI Garcia-Echeverria C, Chene P, Furet P;
XX
DR WPI; 1998-100996/09.
XX
PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT useful in, e.g. diagnosis and treatment of cancer and viral infections
PT and identifying binding agents.
XX
PS Example 1; Page 20; 45pp; English.
XX
CC This is a C-amidated peptide derivative capable of binding to a human
CC oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC molecules that bind to MDM2 and to identify and design inhibitors of
CC MDM2/p53 binding. They may also be used to purify binding partners
CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of

CC cancer and leukaemia patients and for treatment or prevention of disease
CC involving p53/MDM2 interactions, especially tumours and viral infections.
CC The peptides can be administered nasally, rectally, orally or by
CC injection. By interfering with MDM2/p53 interaction, the peptides can
CC activate p53 function and accumulation in normal cells. The peptides
CC which mimic the MDM2 binding site in p53, have a significantly greater
CC blocking activity compared with wild-type p53
XX
SQ Sequence 12 AA;

AAW37196 Length: 12 October 13, 2004 13:39 Type: P Check: 5978 ..
Found using 'claim36' (zara371.key)

```
          |-------|
1       MPRFMDYWEGLN
           3       11
```

---
1 match found in sequence:
aaw37204 ; Human oncogenic protein MDM2 binding biotinylated peptide derivativ
(from "claim36ags.pep")
TOIG of: aaw37204 check: 1571 from: 1 to: 28

ID AAW37204 standard; peptide; 28 AA.
XX
AC AAW37204;
XX
DT 20-JUL-1998 (first entry)
XX
DE Human oncogenic protein MDM2 binding biotinylated peptide derivative 4.
XX
KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW tumour; diagnosis; binding; viral infection; biotinylation.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "biotinylated"
FT Modified-site 28
FT /note= "C-terminal amide"
XX
PN WO9801467-A2.
XX
PD 15-JAN-1998.
XX
PF 04-JUL-1997; 97WO-EP003549.
XX
PR 05-JUL-1996; 96GB-00014197.
PR 07-APR-1997; 97GB-00007041.
XX
PA (NOVS) NOVARTIS AG.
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
PI Garcia-Echeverria C, Chene P, Furet P;
XX
DR WPI; 1998-100996/09.
XX
PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT useful in, e.g. diagnosis and treatment of cancer and viral infections
PT and identifying binding agents.
XX
PS Example 3; Page 21; 45pp; English.
XX
CC This is a biotinylated peptide derivative capable of binding to a human
CC oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC molecules that bind to MDM2 and to identify and design inhibitors of

```
CC   MDM2/p53 binding. They may also be used to purify binding partners
CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
CC   cancer and leukaemia patients and for treatment or prevention of disease
CC   involving p53/MDM2 interactions, especially tumours and viral infections.
CC   The peptides can be administered nasally, rectally, orally or by
CC   injection. By interfering with MDM2/p53 interaction, the peptides can
CC   activate p53 function and accumulation in normal cells. The peptides
CC   which mimic the MDM2 binding site in p53, have a significantly greater
CC   blocking activity compared with wild-type p53
XX
SQ   Sequence 28 AA;

 AAW37204  Length: 28  October 13, 2004 13:39  Type: P  Check: 1571  ..
Found using 'claim36' (zara371.key)

          |-------|
1       SMPRFMDYWEGLNRQIKIWFQNRMKWKK
          4       12

-------
1 match found in sequence:
 aaw37205 ; Human oncogenic protein MDM2 binding biotinylated peptide derivativ
  (from "claim36ags.pep")
  TOIG of: aaw37205  check: 8233  from: 1  to: 31

ID   AAW37205 standard; peptide; 31 AA.
XX
AC   AAW37205;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human oncogenic protein MDM2 binding biotinylated peptide derivative 5.
XX
KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW   tumour; diagnosis; binding; viral infection; biotinylation.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal acetyl"
FT   Modified-site   17
FT                   /label= bAla
FT                   /note= "beta-Alanine"
FT   Modified-site   30
FT                   /label= bAla
FT                   /note= "beta-Alanine"
FT   Modified-site   31
FT                   /note= "biotinylated"
XX
PN   WO9801467-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-EP003549.
XX
PR   05-JUL-1996;   96GB-00014197.
PR   07-APR-1997;   97GB-00007041.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
PI   Garcia-Echeverria C,  Chene P,  Furet P;
XX
DR   WPI; 1998-100996/09.
XX
PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
PT   and identifying binding agents.
XX
PS   Example 3; Page 21; 45pp; English.
XX
CC   This is a biotinylated peptide derivative capable of binding to a human
CC   oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC   molecules that bind to MDM2 and to identify and design inhibitors of
CC   MDM2/p53 binding. They may also be used to purify binding partners
CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
CC   cancer and leukaemia patients and for treatment or prevention of disease
CC   involving p53/MDM2 interactions, especially tumours and viral infections.
CC   The peptides can be administered nasally, rectally, orally or by
CC   injection. By interfering with MDM2/p53 interaction, the peptides can
CC   activate p53 function and accumulation in normal cells. The peptides
CC   which mimic the MDM2 binding site in p53, have a significantly greater
CC   blocking activity compared with wild-type p53
XX
SQ   Sequence 31 AA;

 AAW37205  Length: 31  October 13, 2004 13:39  Type: P  Check: 8233  ..
Found using 'claim36' (zara371.key)

                            |-------|
1       AAVALLPAVLLALLAPXMPRFMDYWEGLNXK
                            20      28

-------
1 match found in sequence:
 aaw37216 ; Human oncogenic protein MDM2 binding peptide derivative 9.
  (from "claim36ags.pep")
  TOIG of: aaw37216  check: 3427  from: 1  to: 9

ID   AAW37216 standard; peptide; 9 AA.
XX
AC   AAW37216;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human oncogenic protein MDM2 binding peptide derivative 9.
XX
KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW   tumour; diagnosis; binding; viral infection.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal acetyl"
FT   Modified-site   9
FT                   /note= "C-terminal amide"
XX
PN   WO9801467-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-EP003549.
XX
PR   05-JUL-1996;   96GB-00014197.
PR   07-APR-1997;   97GB-00007041.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
PI   Garcia-Echeverria C,  Chene P,  Furet P;
XX
DR   WPI; 1998-100996/09.
XX
PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
PT   and identifying binding agents.
```

```
XX
PS   Example 6; Page 26; 45pp; English.
XX
CC   This is a MDM2 binding peptide derivative capable of binding to a human
CC   oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC   inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC   or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC   induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC   p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC   molecules that bind to MDM2 and to identify and design inhibitors of
CC   MDM2/p53 binding. They may also be used to purify binding partners
CC   especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
CC   cancer and leukaemia patients and for treatment or prevention of disease
CC   involving p53/MDM2 interactions, especially tumours and viral infections.
CC   The peptides can be administered nasally, rectally, orally or by
CC   injection. By interfering with MDM2/p53 interaction, the peptides can
CC   activate p53 function and accumulation in normal cells. The peptides
CC   which mimic the MDM2 binding site in p53, have a significantly greater
CC   blocking activity compared with wild-type p53
XX
SQ   Sequence 9 AA;

 AAW37216  Length: 9  October 13, 2004 13:39  Type: P  Check: 3427  ..
Found using 'claim36' (zara371.key)

        |-------|
1       RFMDYWEGL
        1       9

-------
1 match found in sequence:
 aaw37220 ; MDM2 binding peptide unique phage insert sequence 1.
  (from "claim36ags.pep")
  TOIG of: aaw37220  check: 5978  from: 1  to: 12

 ID   AAW37220 standard; peptide; 12 AA.
XX
AC   AAW37220;
XX
DT   20-JUL-1998  (first entry)
XX
DE   MDM2 binding peptide unique phage insert sequence 1.
XX
KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW   tumour; diagnosis; binding; viral infection; phage insert.
XX
OS   Homo sapiens.
XX
PN   WO9801467-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-EP003549.
XX
PR   05-JUL-1996;   96GB-00014197.
PR   07-APR-1997;   97GB-00007041.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
PI   Garcia-Echeverria C,  Chene P,  Furet P;
XX
DR   WPI; 1998-100996/09.
XX
PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
PT   and identifying binding agents.
XX
PS   Example 8; Page 30; 45pp; English.
XX
CC   This is a unique phage insert sequence of the MDM2 binding peptide
CC   identified by phage display. The MDM2 binding peptides and their
CC   derivatives are capable of binding to the human oncogenic protein MDM2.
CC   These peptides can specifically inhibit or block the binding of MDM2 to
CC   the human p53 protein, in vitro or in vivo. Inhibiting the interaction
CC   between the p53 and MDM2 can induce growth arrest or apoptosis in tumour
CC   cells comprising a wild-type p53 and non-elevated levels of MDM2. The
CC   peptides may be used to identify molecules that bind to MDM2 and to
CC   identify and design inhibitors of MDM2/p53 binding. They may also be used
CC   to purify binding partners especially MDM2, diagnose disease by measuring
CC   levels of MDM2 in blood of cancer and leukaemia patients and for
CC   treatment or prevention of disease involving p53/MDM2 interactions,
CC   especially tumours and viral infections. The peptides can be administered
CC   nasally, rectally, orally or by injection. By interfering with MDM2/p53
CC   interaction, the peptides can activate p53 function and accumulation in
CC   normal cells. The peptides which mimic the MDM2 binding site in p53, have
CC   a significantly greater blocking activity compared with wild-type p53
XX
SQ   Sequence 12 AA;

 AAW37220  Length: 12  October 13, 2004 13:39  Type: P  Check: 5978  ..
Found using 'claim36' (zara371.key)

          |-------|
1       MPRFMDYWEGLN
          3       11

-------
1 match found in sequence:
 aaw37221 ; MDM2 binding peptide unique phage insert sequence 2.
  (from "claim36ags.pep")
  TOIG of: aaw37221  check: 6151  from: 1  to: 12

 ID   AAW37221 standard; peptide; 12 AA.
XX
AC   AAW37221;
XX
DT   20-JUL-1998  (first entry)
XX
DE   MDM2 binding peptide unique phage insert sequence 2.
XX
KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW   tumour; diagnosis; binding; viral infection; phage insert.
XX
OS   Homo sapiens.
XX
PN   WO9801467-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-EP003549.
XX
PR   05-JUL-1996;   96GB-00014197.
PR   07-APR-1997;   97GB-00007041.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
PI   Garcia-Echeverria C,  Chene P,  Furet P;
XX
DR   WPI; 1998-100996/09.
XX
PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
PT   and identifying binding agents.
XX
PS   Example 8; Page 30; 45pp; English.
XX
CC   This is a unique phage insert sequence of the MDM2 binding peptide
CC   identified by phage display. The MDM2 binding peptides and their
CC   derivatives are capable of binding to the human oncogenic protein MDM2.
CC   These peptides can specifically inhibit or block the binding of MDM2 to
CC   the human p53 protein, in vitro or in vivo. Inhibiting the interaction
CC   between the p53 and MDM2 can induce growth arrest or apoptosis in tumour
```

CC cells comprising a wild-type p53 and non-elevated levels of MDM2. The
CC peptides may be used to identify molecules that bind to MDM2 and to
CC identify and design inhibitors of MDM2/p53 binding. They may also be used
CC to purify binding partners especially MDM2, diagnose disease by measuring
CC levels of MDM2 in blood of cancer and leukaemia patients and for
CC treatment or prevention of disease involving p53/MDM2 interactions,
CC especially tumours and viral infections. The peptides can be administered
CC nasally, rectally, orally or by injection. By interfering with MDM2/p53
CC interaction, the peptides can activate p53 function and accumulation in
CC normal cells. The peptides which mimic the MDM2 binding site in p53, have
CC a significantly greater blocking activity compared with wild-type p53
XX
SQ Sequence 12 AA;

AAW37221 Length: 12 October 13, 2004 13:39 Type: P Check: 6151 ..
Found using 'claim36' (zara371.key)

```
          |-------|
1       VQNFIDYWTQQF
          3       11
```

---
1 match found in sequence:
aaw37222 ; MDM2 binding peptide unique phage insert sequence 3.
(from "claim36ags.pep")
TOIG of: aaw37222 check: 5993 from: 1 to: 12

ID AAW37222 standard; peptide; 12 AA.
XX
AC AAW37222;
XX
DT 20-JUL-1998 (first entry)
XX
DE MDM2 binding peptide unique phage insert sequence 3.
XX
KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW tumour; diagnosis; binding; viral infection; phage insert.
XX
OS Homo sapiens.
XX
PN WO9801467-A2.
XX
PD 15-JAN-1998.
XX
PF 04-JUL-1997; 97WO-EP003549.
XX
PR 05-JUL-1996; 96GB-00014197.
PR 07-APR-1997; 97GB-00007041.
XX
PA (NOVS) NOVARTIS AG.
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
PI Garcia-Echeverria C, Chene P, Furet P;
XX
DR WPI; 1998-100996/09.
XX
PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT useful in, e.g. diagnosis and treatment of cancer and viral infections
PT and identifying binding agents.
XX
PS Example 8; Page 30; 45pp; English.
XX
CC This is a unique phage insert sequence of the MDM2 binding peptide
CC identified by phage display. The MDM2 binding peptides and their
CC derivatives are capable of binding to the human oncogenic protein MDM2.
CC These peptides can specifically inhibit or block the binding of MDM2 to
CC the human p53 protein, in vitro or in vivo. Inhibiting the interaction
CC between the p53 and MDM2 can induce growth arrest or apoptosis in tumour
CC cells comprising a wild-type p53 and non-elevated levels of MDM2. The
CC peptides may be used to identify molecules that bind to MDM2 and to
CC identify and design inhibitors of MDM2/p53 binding. They may also be used
CC to purify binding partners especially MDM2, diagnose disease by measuring
CC levels of MDM2 in blood of cancer and leukaemia patients and for
CC treatment or prevention of disease involving p53/MDM2 interactions,
CC especially tumours and viral infections. The peptides can be administered
CC nasally, rectally, orally or by injection. By interfering with MDM2/p53
CC interaction, the peptides can activate p53 function and accumulation in
CC normal cells. The peptides which mimic the MDM2 binding site in p53, have
CC a significantly greater blocking activity compared with wild-type p53
XX
SQ Sequence 12 AA;

AAW37222 Length: 12 October 13, 2004 13:39 Type: P Check: 5993 ..
Found using 'claim36' (zara371.key)

```
          |-------|
1       TGPAFTHYWATF
          4       12
```

---
1 match found in sequence:
aaw37223 ; MDM2 binding peptide unique phage insert sequence 4.
(from "claim36ags.pep")
TOIG of: aaw37223 check: 9093 from: 1 to: 15

ID AAW37223 standard; peptide; 15 AA.
XX
AC AAW37223;
XX
DT 20-JUL-1998 (first entry)
XX
DE MDM2 binding peptide unique phage insert sequence 4.
XX
KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW tumour; diagnosis; binding; viral infection; phage insert.
XX
OS Homo sapiens.
XX
PN WO9801467-A2.
XX
PD 15-JAN-1998.
XX
PF 04-JUL-1997; 97WO-EP003549.
XX
PR 05-JUL-1996; 96GB-00014197.
PR 07-APR-1997; 97GB-00007041.
XX
PA (NOVS) NOVARTIS AG.
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
PI Garcia-Echeverria C, Chene P, Furet P;
XX
DR WPI; 1998-100996/09.
XX
PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT useful in, e.g. diagnosis and treatment of cancer and viral infections
PT and identifying binding agents.
XX
PS Example 8; Page 30; 45pp; English.
XX
CC This is a unique phage insert sequence of the MDM2 binding peptide
CC identified by phage display. The MDM2 binding peptides and their
CC derivatives are capable of binding to the human oncogenic protein MDM2.
CC These peptides can specifically inhibit or block the binding of MDM2 to
CC the human p53 protein, in vitro or in vivo. Inhibiting the interaction
CC between the p53 and MDM2 can induce growth arrest or apoptosis in tumour
CC cells comprising a wild-type p53 and non-elevated levels of MDM2. The
CC peptides may be used to identify molecules that bind to MDM2 and to
CC identify and design inhibitors of MDM2/p53 binding. They may also be used
CC to purify binding partners especially MDM2, diagnose disease by measuring
CC levels of MDM2 in blood of cancer and leukaemia patients and for
CC treatment or prevention of disease involving p53/MDM2 interactions,
CC especially tumours and viral infections. The peptides can be administered
CC nasally, rectally, orally or by injection. By interfering with MDM2/p53

```
CC   interaction, the peptides can activate p53 function and accumulation in
CC   normal cells. The peptides which mimic the MDM2 binding site in p53, have
CC   a significantly greater blocking activity compared with wild-type p53
XX
SQ   Sequence 15 AA;

 AAW37223  Length: 15  October 13, 2004 13:39  Type: P  Check: 9093  ..
Found using 'claim36' (zara371.key)

            |-------|
1       IDRAPTFRDHWFALV
            6       14

-------
1 match found in sequence:
 aaw37224 ; MDM2 binding peptide unique phage insert sequence 5.
  (from "claim36ags.pep")
  TOIG of: aaw37224  check: 9428  from: 1  to: 15

 ID   AAW37224 standard; peptide; 15 AA.
 XX
 AC   AAW37224;
 XX
 DT   20-JUL-1998  (first entry)
 XX
 DE   MDM2 binding peptide unique phage insert sequence 5.
 XX
 KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW   tumour; diagnosis; binding; viral infection; phage insert.
 XX
 OS   Homo sapiens.
 XX
 PN   WO9801467-A2.
 XX
 PD   15-JAN-1998.
 XX
 PF   04-JUL-1997;   97WO-EP003549.
 XX
 PR   05-JUL-1996;   96GB-00014197.
 PR   07-APR-1997;   97GB-00007041.
 XX
 PA   (NOVS ) NOVARTIS AG.
 PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
 PI   Garcia-Echeverria C,  Chene P,  Furet P;
 XX
 DR   WPI; 1998-100996/09.
 XX
 PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT   and identifying binding agents.
 XX
 PS   Example 8; Page 30; 45pp; English.
 XX
 CC   This is a unique phage insert sequence of the MDM2 binding peptide
 CC   identified by phage display. The MDM2 binding peptides and their
 CC   derivatives are capable of binding to the human oncogenic protein MDM2.
 CC   These peptides can specifically inhibit or block the binding of MDM2 to
 CC   the human p53 protein, in vitro or in vivo. Inhibiting the interaction
 CC   between the p53 and MDM2 can induce growth arrest or apoptosis in tumour
 CC   cells comprising a wild-type p53 and non-elevated levels of MDM2. The
 CC   peptides may be used to identify molecules that bind to MDM2 and to
 CC   identify and design inhibitors of MDM2/p53 binding. They may also be used
 CC   to purify binding partners especially MDM2, diagnose disease by measuring
 CC   levels of MDM2 in blood of cancer and leukaemia patients and for
 CC   treatment or prevention of disease involving p53/MDM2 interactions,
 CC   especially tumours and viral infections. The peptides can be administered
 CC   nasally, rectally, orally or by injection. By interfering with MDM2/p53
 CC   interaction, the peptides can activate p53 function and accumulation in
 CC   normal cells. The peptides which mimic the MDM2 binding site in p53, have
 CC   a significantly greater blocking activity compared with wild-type p53
 XX
 SQ   Sequence 15 AA;

  AAW37224  Length: 15  October 13, 2004 13:39  Type: P  Check: 9428  ..
 Found using 'claim36' (zara371.key)

             |-------|
1        PRPALVFADYWETLY
             6       14

-------
1 match found in sequence:
 aaw37225 ; MDM2 binding peptide unique phage insert sequence 6.
  (from "claim36ags.pep")
  TOIG of: aaw37225  check: 8833  from: 1  to: 15

 ID   AAW37225 standard; peptide; 15 AA.
 XX
 AC   AAW37225;
 XX
 DT   20-JUL-1998  (first entry)
 XX
 DE   MDM2 binding peptide unique phage insert sequence 6.
 XX
 KW   MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW   tumour; diagnosis; binding; viral infection; phage insert.
 XX
 OS   Homo sapiens.
 XX
 PN   WO9801467-A2.
 XX
 PD   15-JAN-1998.
 XX
 PF   04-JUL-1997;   97WO-EP003549.
 XX
 PR   05-JUL-1996;   96GB-00014197.
 PR   07-APR-1997;   97GB-00007041.
 XX
 PA   (NOVS ) NOVARTIS AG.
 PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI   Lane D,  Boettger V,  Boettger A,  Picksley S,  Hochkeppel H;
 PI   Garcia-Echeverria C,  Chene P,  Furet P;
 XX
 DR   WPI; 1998-100996/09.
 XX
 PT   Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT   useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT   and identifying binding agents.
 XX
 PS   Example 8; Page 30; 45pp; English.
 XX
 CC   This is a unique phage insert sequence of the MDM2 binding peptide
 CC   identified by phage display. The MDM2 binding peptides and their
 CC   derivatives are capable of binding to the human oncogenic protein MDM2.
 CC   These peptides can specifically inhibit or block the binding of MDM2 to
 CC   the human p53 protein, in vitro or in vivo. Inhibiting the interaction
 CC   between the p53 and MDM2 can induce growth arrest or apoptosis in tumour
 CC   cells comprising a wild-type p53 and non-elevated levels of MDM2. The
 CC   peptides may be used to identify molecules that bind to MDM2 and to
 CC   identify and design inhibitors of MDM2/p53 binding. They may also be used
 CC   to purify binding partners especially MDM2, diagnose disease by measuring
 CC   levels of MDM2 in blood of cancer and leukaemia patients and for
 CC   treatment or prevention of disease involving p53/MDM2 interactions,
 CC   especially tumours and viral infections. The peptides can be administered
 CC   nasally, rectally, orally or by injection. By interfering with MDM2/p53
 CC   interaction, the peptides can activate p53 function and accumulation in
 CC   normal cells. The peptides which mimic the MDM2 binding site in p53, have
 CC   a significantly greater blocking activity compared with wild-type p53
 XX
 SQ   Sequence 15 AA;

  AAW37225  Length: 15  October 13, 2004 13:39  Type: P  Check: 8833  ..
 Found using 'claim36' (zara371.key)
```

```
          |-------|
1       PAFSRFWSDLSAGAH
          2       10

-------
1 match found in sequence:
 aaw82320 ; p53 homologue TIP 12/1 peptide.
  (from "claim36ags.pep")
  TOIG of: aaw82320  check: 4400  from: 1  to: 19

 ID   AAW82320 standard; peptide; 19 AA.
 XX
 AC   AAW82320;
 XX
 DT   22-FEB-1999  (first entry)
 XX
 DE   p53 homologue TIP 12/1 peptide.
 XX
 KW   p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.
 XX
 OS   Synthetic.
 XX
 PN   WO9847525-A1.
 XX
 PD   29-OCT-1998.
 XX
 PF   20-APR-1998;   98WO-GB001144.
 XX
 PR   22-APR-1997;   97GB-00008092.
 XX
 PA   (UYDU-) UNIV DUNDEE.
 XX
 PI   Lane DP;
 XX
 DR   WPI; 1998-609932/51.
 XX
 PT   New agents which inhibit interaction of p53 and mdm2 - useful for
 PT   activating p53, e.g. for treating cancers, viral conditions or other
 PT   conditions associated with non functional p53 or mdm2.
 XX
 PS   Disclosure; Fig 1; 52pp; English.
 XX
 CC   This sequence is a peptide homologue of a region of p53 which binds to
 CC   mdm2. This peptide is used in the construction of a novel agent capable
 CC   of disrupting the binding of p53 and mdm2 or inhibiting the production of
 CC   mdm2 in a population of cells. This agent is also used in the preparation
 CC   of a therapeutic for activating p53, where the population of cells do not
 CC   overexpress mdm2. Inhibiting mdm2 production and/or inhibiting the
 CC   binding of mdm2 to p53 allows levels of p53 to increase by reducing the
 CC   clearance of p53 by mdm2, and can be used to activate p53 function. The
 CC   agents for use in therapeutics for activating p53 can be used for the
 CC   treatment of cancer, viral conditions or other conditions associated with
 CC   non-functional p53
 XX
 SQ   Sequence 19 AA;

  AAW82320  Length: 19  October 13, 2004 13:39  Type: P  Check: 4400  ..
 Found using 'claim36' (zara371.key)

              |-------|
1         PPLSMPRFMDYWEGLNENG
              7       15

-------
1 match found in sequence:
 aaw82322 ; p53 homologue TIP 12/1 peptide.
  (from "claim36ags.pep")
  TOIG of: aaw82322  check: 4400  from: 1  to: 19

 ID   AAW82322 standard; peptide; 19 AA.
 XX
 AC   AAW82322;
 XX
 DT   22-FEB-1999  (first entry)
 XX
 DE   p53 homologue TIP 12/1 peptide.
 XX
 KW   p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.
 XX
 OS   Synthetic.
 XX
 PN   WO9847919-A1.
 XX
 PD   29-OCT-1998.
 XX
 PF   20-APR-1998;   98WO-GB001140.
 XX
 PR   22-APR-1997;   97GB-00008089.
 XX
 PA   (UYDU-) UNIV DUNDEE.
 XX
 PI   Lane DP;
 XX
 DR   WPI; 1998-609975/51.
 XX
 PT   New substance with a mdm2 binding domain and coupling partner - useful
 PT   for stabilising in cells without an efficient mdm2-mediated degradation
 PT   pathway.
 XX
 PS   Disclosure; Fig 1; 52pp; English.
 XX
 CC   This sequence is a peptide homologue of a region of p53 which binds to
 CC   mdm2. This peptide is used in the construction of a novel agent capable
 CC   of disrupting the binding of p53 and mdm2 or inhibiting the production of
 CC   mdm2 in a population of cells. This agent is also used in the preparation
 CC   of a therapeutic for activating p53, where the population of cells do not
 CC   overexpress mdm2. Inhibiting mdm2 production and/or inhibiting the
 CC   binding of mdm2 to p53 allows levels of p53 to increase by reducing the
 CC   clearance of p53 by mdm2, and can be used to activate p53 function. The
 CC   agents for use in therapeutics for activating p53 can be used for the
 CC   treatment of cancer, viral conditions or other conditions associated with
 CC   non-functional p53
 XX
 SQ   Sequence 19 AA;

  AAW82322  Length: 19  October 13, 2004 13:39  Type: P  Check: 4400  ..
 Found using 'claim36' (zara371.key)

              |-------|
1         PPLSMPRFMDYWEGLNENG
              7       15

-------
1 match found in sequence:
 abb65993 ; Drosophila melanogaster polypeptide SEQ ID NO 24771.
  (from "claim36ags.pep")
  TOIG of: abb65993  check: 1097  from: 1  to: 1075

 ID   ABB65993 standard; protein; 1075 AA.
 XX
 AC   ABB65993;
 XX
 DT   26-MAR-2002  (first entry)
 XX
 DE   Drosophila melanogaster polypeptide SEQ ID NO 24771.
 XX
 KW   Drosophila; developmental biology; cell signalling; insecticide;
 KW   pharmaceutical.
 XX
 OS   Drosophila melanogaster.
 XX
 PN   WO200171042-A2.
 XX
 PD   27-SEP-2001.
 XX
```

PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL10096.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 24771; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1075 AA;

ABB65993 Length: 1075 October 13, 2004 13:39 Type: P Check: 1097 ..
Found using 'claim36' (zara371.key)

...

|-------|
451 VPVKDICQSGNTNITMCPLCDWCNFWDLKETCNYAKVTYLIDNPSTVFFAVFMSFWATLF
501 509

511 LELWKRYSAEITHRWDLTGFDVHEEHPRPQYLARLEHIPPTRVDYVTNI

...

---
1 match found in sequence:
abb73174 ; Mdm/hdm antagonist peptide SEQ ID NO:135.
(from "claim36ags.pep")
TOIG of: abb73174 check: 5978 from: 1 to: 12

ID ABB73174 standard; peptide; 12 AA.
XX
AC ABB73174;
XX
DT 05-APR-2002 (first entry)
XX
DE Mdm/hdm antagonist peptide SEQ ID NO:135.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Claim 39; Page 53; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 12 AA;

ABB73174 Length: 12 October 13, 2004 13:39 Type: P Check: 5978 ..
Found using 'claim36' (zara371.key)

|-------|
1 MPRFMDYWEGLN
3 11

---
1 match found in sequence:
abb73175 ; Mdm/hdm antagonist peptide SEQ ID NO:136.
(from "claim36ags.pep")
TOIG of: abb73175 check: 6151 from: 1 to: 12

ID ABB73175 standard; peptide; 12 AA.
XX
AC ABB73175;
XX
DT 05-APR-2002 (first entry)
XX
DE Mdm/hdm antagonist peptide SEQ ID NO:136.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;

KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Claim 39; Page 53; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 12 AA;

ABB73175 Length: 12 October 13, 2004 13:39 Type: P Check: 6151 ..
Found using 'claim36' (zara371.key)

|-------|
1 VQNFIDYWTQQF
3 11

---
1 match found in sequence:
abb73176 ; Mdm/hdm antagonist peptide SEQ ID NO:137.
(from "claim36ags.pep")
TOIG of: abb73176 check: 5993 from: 1 to: 12

ID ABB73176 standard; peptide; 12 AA.
XX
AC ABB73176;
XX
DT 05-APR-2002 (first entry)

XX
DE Mdm/hdm antagonist peptide SEQ ID NO:137.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Claim 39; Page 53; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 12 AA;

ABB73176 Length: 12 October 13, 2004 13:39 Type: P Check: 5993 ..
Found using 'claim36' (zara371.key)

|-------|
1 TGPAFTHYWATF
4 12

---
1 match found in sequence:

```
abb73177 ; Mdm/hdm antagonist peptide SEQ ID NO:138.
 (from "claim36ags.pep")
 TOIG of: abb73177  check: 9093  from: 1  to: 15

ID   ABB73177 standard; peptide; 15 AA.
XX
AC   ABB73177;
XX
DT   05-APR-2002  (first entry)
XX
DE   Mdm/hdm antagonist peptide SEQ ID NO:138.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C;  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Claim 39; Page 53; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 15 AA;

 ABB73177  Length: 15  October 13, 2004 13:39  Type: P  Check: 9093  ..
Found using 'claim36' (zara371.key)

             |-------|
1        IDRAPTFRDHWFALV
             6       14

-------
1 match found in sequence:
abb73178 ; Mdm/hdm antagonist peptide SEQ ID NO:139.
 (from "claim36ags.pep")
 TOIG of: abb73178  check: 9428  from: 1  to: 15

ID   ABB73178 standard; peptide; 15 AA.
XX
AC   ABB73178;
XX
DT   05-APR-2002  (first entry)
XX
DE   Mdm/hdm antagonist peptide SEQ ID NO:139.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Claim 39; Page 53; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
```

```
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 15 AA;

 ABB73178  Length: 15  October 13, 2004 13:39  Type: P  Check: 9428  ..
Found using 'claim36' (zara371.key)

            |-------|
1       PRPALVFADYWETLY
            6       14

-------
1 match found in sequence:
 abb73179 ; Mdm/hdm antagonist peptide SEQ ID NO:140.
  (from "claim36ags.pep")
  TOIG of: abb73179  check: 8833  from: 1  to: 15

ID   ABB73179 standard; peptide; 15 AA.
XX
AC   ABB73179;
XX
DT   05-APR-2002  (first entry)
XX
DE   Mdm/hdm antagonist peptide SEQ ID NO:140.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Claim 39; Page 53; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 15 AA;

 ABB73179  Length: 15  October 13, 2004 13:39  Type: P  Check: 8833  ..
Found using 'claim36' (zara371.key)

            |-------|
1       PAFSRFWSDLSAGAH
            2       10

-------
1 match found in sequence:
 abb92234 ; Herbicidally active polypeptide SEQ ID NO 1445.
  (from "claim36ags.pep")
  TOIG of: abb92234  check: 9732  from: 1  to: 440

ID   ABB92234 standard; protein; 440 AA.
XX
AC   ABB92234;
XX
DT   31-MAY-2002  (first entry)
XX
DE   Herbicidally active polypeptide SEQ ID NO 1445.
XX
KW   Herbicidal; plant; agriculture; herbicide.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200210210-A2.
XX
PD   07-FEB-2002.
XX
PF   28-AUG-2001; 2001WO-EP009892.
XX
PR   28-AUG-2001; 2001WO-EP009892.
XX
PA   (FARB ) BAYER AG.
XX
PI   Tietjen K,  Weidler M;
XX
DR   WPI; 2002-269010/31.
XX
PT   Identifying plant target proteins for herbicidally active compounds,
PT   comprising aligning and comparing nucleic acid or amino acid sequences
PT   from plant with nucleic acid or amino acid sequences from non-plant
PT   organisms.
XX
PS   Claim 5; SEQ ID NO 1445; 261pp + Sequence Listing; English.
XX
CC   The invention relates to identifying target proteins (ABB90790-ABB94016)
CC   for herbicidally active compounds, comprising aligning and comparing
CC   nucleic acid or amino acid sequences from plant with nucleic acid or
CC   amino acid sequences from non-plant organisms using suitable search
CC   parameters, where plant sequences having an E-value greater by a factor
CC   of 3 than the E-value of most similar non-plant sequences are selected.
CC   The polypeptides or nucleic acids encoding them are useful for
CC   identifying modulators. The identified modulators are useful as
CC   herbicides
```

```
XX
SQ   Sequence 440 AA;

ABB92234  Length: 440  October 13, 2004 13:39  Type: P  Check: 9732  ..
Found using 'claim36' (zara371.key)

...

                                                                |-------|
350      KTEYKESLPAPENNDLYKGKIWCVGNNTCDPIQRGGPCQKPDLTVLHASYAFSSYWAQFR
                                                               400     408

410      KIGGTCSFNGLATQTIKDPSYGRCEFPSVTL

-------
1 match found in sequence:
 abb92409 ; Herbicidally active polypeptide SEQ ID NO 1620.
  (from "claim36ags.pep")
  TOIG of: abb92409  check: 2170  from: 1  to: 476

 ID   ABB92409 standard; protein; 476 AA.
 XX
 AC   ABB92409;
 XX
 DT   31-MAY-2002  (first entry)
 XX
 DE   Herbicidally active polypeptide SEQ ID NO 1620.
 XX
 KW   Herbicidal; plant; agriculture; herbicide.
 XX
 OS   Arabidopsis thaliana.
 XX
 PN   WO200210210-A2.
 XX
 PD   07-FEB-2002.
 XX
 PF   28-AUG-2001; 2001WO-EP009892.
 XX
 PR   28-AUG-2001; 2001WO-EP009892.
 XX
 PA   (FARB ) BAYER AG.
 XX
 PI   Tietjen K,  Weidler M;
 XX
 DR   WPI; 2002-269010/31.
 XX
 PT   Identifying plant target proteins for herbicidally active compounds,
 PT   comprising aligning and comparing nucleic acid or amino acid sequences
 PT   from plant with nucleic acid or amino acid sequences from non-plant
 PT   organisms.
 XX
 PS   Claim 5; SEQ ID NO 1620; 261pp + Sequence Listing; English.
 XX
 CC   The invention relates to identifying target proteins (ABB90790-ABB94016)
 CC   for herbicidally active compounds, comprising aligning and comparing
 CC   nucleic acid or amino acid sequences from plant with nucleic acid or
 CC   amino acid sequences from non-plant organisms using suitable search
 CC   parameters, where plant sequences having an E-value greater by a factor
 CC   of 3 than the E-value of most similar non-plant sequences are selected.
 CC   The polypeptides or nucleic acids encoding them are useful for
 CC   identifying modulators. The identified modulators are useful as
 CC   herbicides
 XX
 SQ   Sequence 476 AA;

 ABB92409  Length: 476  October 13, 2004 13:39  Type: P  Check: 2170  ..
 Found using 'claim36' (zara371.key)

...

                                                                |-------|
386      VWCVAVDGADEAELGQALNFACGRSNATCAALAPGGECYAPVTVTWHASYAFSSYWAQFR
                                                               436     444

446      NQSSQCYFNGLARETTTNPGNERCKFPSVTL

-------
1 match found in sequence:
 adb61841 ; Peptide Seq ID81 related to inhibitors of apoptosis.
  (from "claim36ags.pep")
  TOIG of: adb61841  check: 3739  from: 1  to: 29

 ID   ADB61841 standard; peptide; 29 AA.
 XX
 AC   ADB61841;
 XX
 DT   04-DEC-2003  (first entry)
 XX
 DE   Peptide Seq ID81 related to inhibitors of apoptosis.
 XX
 KW   baculovirus inhibitor of apoptosis repeat domain; BIR domain;
 KW   apoptosis pathway; embryonic development; viral pathogenesis; cancer;
 KW   autoimmune disorder; neurodegenerative disease; apoptotic response;
 KW   systemic lupus erythematosis; multiple sclerosis; viral infection;
 KW   herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
 KW   HIAP1; cIAP2; HIAP2; cIAP1; RING zinc finger; caspase-3; caspase-7;
 KW   caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;
 KW   cervical cancer; uterine cancer; testicular cancer;
 KW   small cell lung carcinoma; uterine cancer; renal cell carcinoma;
 KW   Wilm's tumour.
 XX
 OS   Unidentified.
 XX
 PN   WO2003040172-A2.
 XX
 PD   15-MAY-2003.
 XX
 PF   12-NOV-2002; 2002WO-CA001738.
 XX
 PR   09-NOV-2001; 2001US-0332300P.
 PR   08-APR-2002; 2002US-0370934P.
 XX
 PA   (AEGE-) AEGERA THERAPEUTICS INC.
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 PI   Boudreault A,  Korneluk RG,  La Casse E,  Liston P;
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 DR   WPI; 2003-513532/48.
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 PT   Polypeptide capable of forming a complex with a polypeptide comprising a
 PT   baculovirus inhibitor of apoptosis repeat domain useful for treating
 PT   cancer and other neoplasms.
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 PS   Disclosure; Page 13; 53pp; English.
 XX
 CC   This invention relates to a substantially pure polypeptide having a
 CC   length of less than 100 amino acids and capable of forming a complex with
 CC   a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
 CC   (BIR) domain. The apoptosis pathway is known to play a critical role in
 CC   embryonic development, viral pathogenesis, cancer, autoimmune disorders
 CC   and neurodegenerative diseases. The failure of the apoptotic response has
 CC   been implicated in the development of cancer, autoimmune disorders (for
 CC   example systemic lupus erythematosis and multiple sclerosis) and viral
 CC   infections (including herpes virus, poxvirus and adenovirus. The
 CC   inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
 CC   more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
 CC   (cIAP2) and HIAP2 (cIAP1) all posses three BIR domains and carboxy
 CC   terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
 CC   -9 which are proteases involved in the initiation of apoptosis. Compounds
 CC   which inhibit the activity of IAPs may therefore have cytostatic activity
 CC   through the enhancement of apoptosis. The polypeptides of the invention
 CC   are candidate peptide ligands for binding to the BIR domain of IAPs. They
 CC   may be useful for the treatment of cancer and other neoplasms, such as
 CC   leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
 CC   cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
 CC   and Wilm's tumour, and for enhancing apoptosis. The present sequence is
 CC   that of a peptide which is suggested as a possible peptide for fusing to
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CC the IAP protein BIR domain-binding peptides of the invention.
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SQ Sequence 29 AA;

ADB61841 Length: 29 October 13, 2004 13:39 Type: P Check: 3739 ..
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